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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:13:30 ; Search time 33.1474 Seconds  
(without alignments)  
1045.185 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350  
Sequence: 1 KPDMESEMDPDLQERYD.....KPRKNPEVSTLRKLYIQ 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: A\_Geneseq\_101002.\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
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19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
24: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1350	100.0	281	20	AAW93592
2	1350	100.0	281	21	AAW93213
3	1332	98.7	257	21	AAW68864
4	940.5	69.7	242	21	AAW93214
5	940.5	69.7	242	23	AAW77980
6	912.5	67.6	242	23	AAW77984
7	892.5	66.1	229	21	AAW68865
8	804.5	59.6	214	21	AAW93216
9	692.5	51.3	230	21	AAW93215
10	427	31.6	234	23	AAW72882

11	286.5	21.2	261	22	AAE0610
12	276.5	20.5	452	23	ABW10110
13	276	20.4	277	22	AAW05395
14	275.5	20.4	435	17	AAW90703
15	274.5	20.3	435	16	AAW64771
16	274.5	20.3	435	17	AAW98462
17	274.5	20.3	435	18	AAW26274
18	274.5	20.3	435	18	AAW21716
19	274.5	20.3	435	21	AAW14257
20	274.5	20.3	435	22	AAW00599
21	274.5	20.3	435	23	ABW01217
22	274.5	20.3	435	16	AAW64768
23	274.5	20.3	441	21	AAW14253
24	274	20.3	277	17	AAW00372
25	274	20.3	277	17	AAW00677
26	274	20.3	277	17	AAW95831
27	274	20.3	277	19	AAW47089
28	274	20.3	277	19	AAW41688
29	273	20.2	277	17	AAW16600
30	273	20.2	277	20	AAW21717
31	273	20.2	277	22	AAW78712
32	273	20.2	277	22	AAW05394
33	273	20.2	277	22	AAW00600
34	273	20.2	277	23	ABW01218
35	271	20.1	249	21	AAW26763
36	269	19.9	241	22	AAW98654
37	268.5	19.9	245	22	AAW95979
38	265	19.6	503	21	AAW14247
39	264	19.6	277	19	AAW48945
40	264	19.6	277	19	AAW48937
41	263.5	19.5	497	21	AAW14248
42	260.5	19.3	435	21	AAW14262
43	259	19.2	505	15	AAW47463
44	256	19.0	503	15	AAW45289
45	255.5	18.9	303	18	AAW15247

#### ALIGNMENTS

RESULT 1	
AAW93592	AAW93592 standard; Protein; 281 AA.
XX	XX
AC	AAW93592;
XX	XX
DT	21-JUN-1999 (first entry)
XX	XX
DE	Mouse caspase-14 protein.
XX	XX
KW	Caspase-14; murine; protease; treatment; apoptotic-related disease;
KW	autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
KW	neurodegenerative disease; ischemic injury; anti-idiotypic antibody;
KW	caspase-14 processing activity; epitope; competitor; modulator.
XX	XX
OS	Mus gp.
PN	XX
XX	W09910504-A2.
XX	XX
PD	04-MAR-1999.
XX	XX
PF	26-AUG-1998; 98WO-US17715.
XX	XX
PR	26-AUG-1997; 97US-0056986.
XX	XX
PI	(IDUN-) IDUN PHARM INC.
XX	XX
PI	Alnemri ES, Fernandes-Alnemri T;
XX	XX
DR	WPI: 1999-204670/17.
DR	N-PSDB; AAX23515.
XX	XX
PT	Newly isolated polynucleotide encoding a caspase-14 polypeptide

PT useful for identifying (ant)agonists that are useful in the  
PT diagnosis and treatment of apoptosis-related diseases

PS Claim 4, Fig 1, 59pp; English.

XX This invention describes a novel murine caspase-14 which has protease  
CC activity. The caspase-14 polypeptide is useful for identifying  
CC (ant)agonists of the polypeptide, where enzyme activity is measured  
CC with a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated  
CC caspase-14 is useful for identifying inhibitors or enhancers of  
CC caspase-14 activity. The compounds identified by both methods  
CC form pharmaceutical compositions for treating apoptotic-related diseases,  
CC including autoimmune disease, cancer, acquired immunodeficiency syndrome  
CC (AIDS), neurodegenerative diseases and ischemic injury. The  
CC anti-caspase-14 antibody is useful for measuring the level of caspase-14  
CC in a tissue sample. An antibody that binds to a caspase-14 polypeptide is  
CC useful for isolating the polypeptide, and an antibody that binds to the  
CC large or small subunit the polypeptide is useful for identifying samples  
CC heterodimer or heterotrimer activity. An antibody that binds to caspase-14  
CC apoptotic activity or in a screening assay to identify (ant)agonists. The  
CC antibodies form kits for such purposes. The anti-caspase-14 antibody is  
CC also useful for preparing anti-idiotypic antibodies, which mimic a  
CC caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,  
CC the antibody is useful as a competitor of caspase-14 in reducing the  
CC level of caspase-14 activity, which reduces the level of apoptotic  
CC activity. Oligonucleotides made from the polynucleotides are useful as  
CC polymerase chain reaction (PCR) primers or probes to screen genomic or  
CC cDNA libraries for similar caspase-14 encoding polynucleotides, or for  
CC diagnosis of diseases associated with enhanced or inhibited apoptosis.  
CC The isolated caspase-14 gene permits methods of modulating apoptosis  
CC for the treatment of human diseases.

XX Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 20; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.5e-130;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARBSSEVDMELERMFYLKFEESTWK 60  
DB 17 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARBSSEVDMELERMFYLKFEESTWK 76  
QY 61 RDPYTAQOFLBELDEFQOITIDNWEPEVSCAFVYLMHAGEGLKGDEKVRLEDFEVLN 120  
DB 77 RDPYTAQOFLBELDEFQOITIDNWEPEVSCAFVYLMHAGEGLKGDEKVRLEDFEVLN 136  
QY 121 NNKCALRGKPKRYVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 180  
DB 137 NNKCALRGKPKRYVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 196  
QY 181 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFPIHKKSILELBEITRLMANTVEMOEG 240  
DB 197 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFPIHKKSILELBEITRLMANTVEMOEG 256  
QY 241 KPRKYNPEVOSTLRKKLYIQ 260  
DB 257 KPRKYNPEVOSTLRKKLYIQ 276

RESULT 2  
AA93213  
ID AA93213 standard; Protein; 281 AA.

XX AA93213;

XX 04-SEP-2000 (first entry)

XX Amino acid sequence of a murine caspase-14.

XX Caspase-14; cell death specific protease; apoptosis stimulator;  
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

XX

OS Mus sp.

XX Key Location/Qualifiers  
FT Region 1..156 /note="large subunit"

FT Active-site 134..138  
FT Cleavage-site 156..157  
FT Region 163..163  
FT /note="small subunit"

XX MO200028047-A1.

XX 18-MAY-2000.

XX 29-OCT-1999; 99MO-US25523.

XX 06-NOV-1998; 98US-0187789.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

XX WPI; 2000-376558/32.

XX N-PSDB; AAA15163.

XX Novel nucleic acids encoding cell death specific protease termed

XX caspase-14 useful for treating cancers by stimulating apoptosis

XX Claim 52, Fig 1, 78pp; English.

XX The present sequence represents a murine caspase-14 polypeptide. The  
CC polypeptide is a cell death specific protease, and is an apoptosis  
CC stimulator. Caspase-14 polynucleotides and polypeptides, and  
CC anti-caspase-14 antibodies are useful for treating or reducing the  
CC severity of pathological conditions associated with increased or  
CC decreased levels of apoptosis. Apoptosis mediated diseases such as  
CC AIDS, neurodegenerative diseases and ischemic injury are treated by  
CC administering anti-caspase-14 antibodies. The antibody is useful for  
CC determining the presence or the level of caspase-14 in tissue sample  
CC and also for the isolation of caspase-14 with apoptotic activity or  
CC in screening assay to identify an agent that inhibits heterodimer or  
CC heterotrimer formation and therefore, apoptosis.

XX Sequence 281 AA;

Query Match 100.0%; Score 1350; DB 21; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2.5e-130;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARBSSEVDMELERMFYLKFEESTWK 60  
DB 17 KPDSEMSDPOLOEERYDMSGARLALTLCVTKARBSSEVDMELERMFYLKFEESTWK 76  
QY 61 RDPYTAQOFLBELDEFQOITIDNWEPEVSCAFVYLMHAGEGLKGDEKVRLEDFEVLN 120  
DB 77 RDPYTAQOFLBELDEFQOITIDNWEPEVSCAFVYLMHAGEGLKGDEKVRLEDFEVLN 136  
QY 121 NNKCALRGKPKRYVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 180  
DB 137 NNKCALRGKPKRYVYIIQACRGEHRDPGEBELRGNEBELGDEBELGDEVAVLKNPPOSIFTY 196  
QY 181 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFPIHKKSILELBEITRLMANTVEMOEG 240  
DB 197 TDTLHIYSTVEGYLSYRDEKSGSFIQTLTVDFPIHKKSILELBEITRLMANTVEMOEG 256  
QY 241 KPRKYNPEVOSTLRKKLYIQ 260  
DB 257 KPRKYNPEVOSTLRKKLYIQ 276

RESULT 3  
AA93213

ID	AA	6864	standard; Protein; 257 AA.
XX	AA	6864;	
XX	DT	16-MAY-2000	(first entry)
XX	DE	Amino acid sequence of a murine caspase-1-like polypeptide.	
XX	KM	Mouse; caspase-1-like polypeptide; human; caspase; apoptosis;	
XX	XX	skin disease; keratinisation; wound healing.	
XX	OS	Mus musculus.	
XX	XX	MO200004169-A1.	
PN	PD	27-JAN-2000.	
XX	PF	12-JUL-1999; 99MO-EP04939.	
XX	PR	17-JUL-1998; 98EP-0202422.	
XX	PA	(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.	
PI	PI	Van De Craen M, Declercq W, Vandenabeele P, Fiers W;	
XX	DR	WPI; 2000-182433/16.	
XX	DR	N-PSDB; AA260683.	
PT	PT	New murine and human caspase homologues useful for treating skin	
XX	XX	related disorders -	
PS	PS	Claim 1; Page 51-52; 68pp; English.	
XX	XX	The present sequence represents a murine caspase-1-like polypeptide. The	
CC	CC	specificity also describes a human caspase-1-like polypeptide.	
CC	CC	Caspases are cysteinyl aspartate-specific proteinases which play a	
CC	CC	central role in apoptosis. The polypeptides of the invention are related	
CC	CC	to human and murine caspase-2 and human caspase-9, and possess all of	
CC	CC	the typical amino acids involved in catalysis, including the QACRG box,	
CC	CC	and contain no or only a very short prodomain. mRNA expression of the	
CC	CC	homologues of the invention is predominant in the skin. The caspase-1-like	
CC	CC	polypeptides are useful for treating human or animal diseases, such	
CC	CC	as skin diseases. They are also useful for screening for compounds that	
CC	CC	modulate its activity, i.e. agonists, antagonists, and inhibitors. The	
CC	CC	caspase-1-like polypeptides and polynucleotides are useful for modulating	
CC	CC	keratinisation, for diagnosing and treating inappropriate wound	
CC	CC	healing.	
SO	SO	Sequence 257 AA;	
Query Match	98.7%;	Score 1332;	DB 21; Length 257;
Best Local Similarity	100.0%;	Pred. No. 1.6e-128;	
Matches 257;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
4	MESEMSDPLOEERDYSNGARLALTLCYTKARBSGEVDMELERMFYLRKEESTMKRDP	63	
1	MESEMSDPLOEERDYSNGARLALTLCYTKARBSGEVDMELERMFYLRKEESTMKRDP	60	
64	TAQQLLEELDEFOOTIDNNEBPVSCAFVVLMAHGEESGLLKGBDEKVRLEDIPEVYLNKN	123	
61	TAQQLLEELDEFOOTIDNNEBPVSCAFVVLMAHGEESGLLKGBDEKVRLEDIPEVYLNKN	120	
124	CAALGKPKVYIIQACRGHRDPGEELRNGEELGDEELGDEGVAVLKNPPOSIPYTYDT	183	
121	CAALGKPKVYIIQACRGHRDPGEELRNGEELGDEELGDEGVAVLKNPPOSIPYTYDT	180	
184	LHIYSTVEGYLSYRHDKEKSGFIQITLTVFIHKKSILTEITRLMANTVMEQEKR	243	
181	LHIYSTVEGYLSYRHDKEKSGFIQITLTVFIHKKSILTEITRLMANTVMEQEKR	240	
244	KNPEVOSTLRKKLYIQ	260	
241	KNPEVOSTLRKKLYIQ	257	

XX	AAV93214; standard; Protein: 242 AA.
XX	AAV93214
XX	AAV93214;
XX	04-SEP-2000 (first entry)
XX	Amino acid sequence of a human caspase-14.
XX	Caspase-14; cell death specific protease; apoptosis stimulator;
XX	Apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX	Homo sapiens.
XX	Key
XX	Region
XX	Location/Qualifiers
XX	1..146
XX	/note= "large subunit"
XX	Active-site
XX	130..134
XX	Cleavage-site
XX	146..147
XX	Region
XX	147..242
XX	/note= "small subunit"
XX	WO200028047-A1.
XX	18-MAY-2000.
XX	29-OCT-1999; 99WO-US25523.
XX	06-NOV-1998; 98US-0187789.
XX	(UYJE-) UNIV JEFFERSON THOMAS.
XX	Alnemri ES, Fernandez-Alnemri T;
XX	WPI: 2000-376556/32.
XX	N-PSDB; AAA15164.
XX	Novel nucleic acids encoding cell death specific protease termed
XX	caspase-14 useful for treating cancers by stimulating apoptosis -
XX	Claim 13; Fig 7; 79pp; English.
XX	The present sequence represents a human caspase-14 polypeptide. The
XX	polypeptide is a cell death specific protease, and is an apoptosis
XX	stimulator. Caspase-14 polynucleotides and polypeptides, and
XX	anti-caspase-14 antibodies are useful for treating or reducing the
XX	severity of pathological conditions associated with increased or
XX	decreased levels of apoptosis. Apoptosis mediated diseases such as
XX	AIDS, neurodegenerative diseases and ischemic injury are treated by
XX	administering anti-caspase-14 antibodies. The antibody is useful for
XX	determining the presence or the level of caspase-14 in tissue sample
XX	and also for the isolation of caspase-14 with apoptotic activity or
XX	in screening assay to identify an agent that inhibits heterodimer or
XX	heterotetramer formation and therefore, apoptosis.
XX	Sequence 242 AA;
XX	Query Match 69.7%; Score 940.5; DB 21; Length 242;
XX	Best Local Similarity 71.3%; Pred. No. 2,8e-86;
XX	Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps
XX	8 MSDPPOLOBERYDMSGARLALTLCYTKAREGSEVMEALERMFRILKRESTMKRPDPAQ 67
XX	1 MSNPRLSEEEKYDMSGARLALTLCYTKAREGSEEDLDLLEHMFQLRRESTMKRPDPAQ 60
XX	68 FLEELDEEFOOTIDNNEEPVSCAFVLLMHGEGGLKGDGKDEKVRLEDPEVLLNNKNCAL 127
XX	61 FOELERKQOALIDSNEDEVSCAFVLLMHGREGFLKGDGDEVKLENLFELANNKNCAL 120
XX	128 RCKPKVYIIQACRGSHRDPGEELRNGEELGDEELGDE-VAVLLNNPQSIPTVYTDLTHI 186





Query Match	67.6%	Score 912.5	DB 23	Length 242
Best Local Similarity	71.8%	Pred. No. 2.1e-85		
Matches 176	Conservative 28	Mismatches 28	Indels 13	Gaps 2
QY	17	ERYDMSGARILTLTCTVKAREGSEVDMELLEMFRYLKRESTMKDPDTAQQGLEBELDERQ	76	
	10	EKYDMSGARILTLTCTVKAREGSEEDDLALHEMFQRLPRESMTKDDPTAEOEQEBELKQ	69	
QY	77	QTIDMEEPVSCAFVYLMAHGEGLKGEDEQGVLEDFEVLNNKNCALGKPKPVYII	136	
Db	70	QAIDREDPVSCAFVYLMAHGEGLKGEDEGMVLELTFEALNNKNCALGKPKPVYII	129	
QY	137	QACRGHNRPGBELRGNEELGDEBELGDE-VAVLKNNPQSIPTYDTLHISTVEGYLS	195	
Db	130	QACGGEQGRDPG-----ETVGDGEIMVLIKDSQTIPTTDLAHVISTVEGYIA	177	
QY	196	YRHDEKSGSFIQTLTDVFIHKKGSLLELTBEITRLMANTEVQESKPRKNDPEVOSTLRK	255	
Db	178	YRHDKGSGSFIQTLTDVDFETKRGHILLELTBEITRMAEALVQEGKARKTNEIDOSTLRK	237	
QY	256	KLYLQ 260		
Db	238	RLYLQ 242		

XX	RESULT 7
XX	AAV68865
XX	AAV68865 standard; Protein; 229 AA.
XX	
XX	AAV68865;
XX	
XX	16-MAY-2000 (first entry)
XX	
XX	Amino acid sequence of a human caspase-1-like polypeptide.
XX	
XX	Mouse; caspase-1-like polypeptide; human; caspase; apoptosis;
XX	skin disease; keratinisation; wound healing.
XX	
XX	Homo sapiens.
XX	
XX	WO200004169-A1.
XX	
XX	27-JAN-2000.
XX	
XX	12-JUL-1999; 99WO-EP04939.
XX	
XX	17-JUL-1998; 98EP-0202422.
XX	
XX	(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX	
XX	Van De Craen M, Declercq W, Vandenaabeele P, Fiers W;
XX	
XX	WPI; 2000-182433/16.
XX	
XX	N-PSDB; AAZ60684.
XX	
XX	New murine and human caspase homologues useful for treating skin
XX	related disorders -
XX	
XX	Claim 2; Page 53-54; 68pp; English.
XX	
XX	The present sequence represents a human caspase-1-like polypeptide.
XX	The specification also describes a murine caspase-1-like polypeptide.
XX	Caspases are cysteinyl aspartate-specific proteinases which play a
XX	central role in apoptosis. The polypeptides of the invention are related
XX	to human and murine caspase-2 and human caspase-9, and possess all of
XX	the typical amino acids involved in catalysis, including the QACRG box,
XX	and contain no or only a very short prodomain. mRNA expression of the
XX	homologues of the invention is predominant in the skin. The caspase-1-like
XX	polypeptides are useful for treating human or animal diseases, such
XX	as skin diseases. They are also useful for screening for compounds that
XX	modulate its activity, i.e. agonists, antagonists, and inhibitors. The
XX	caspase-1-like polypeptides and polynucleotides are useful for modulating
XX	keratinisation, for diagnosing and treating inappropriate wound

[illegible]

RESULT 8	
AA193216	
ID	AA193216 standard; Protein, 214 AA.
XX	
AC	AA193216;
XX	
DT	04-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of a human caspase-14 splice variant.
XX	
KW	Caspase-14; cell death specific protease; apoptosis stimulator;
KW	apoptosis; AIDS; neurodegenerative disease; ischemic injury.
OS	
XX	
XX	Homo sapiens.
XX	
FT	Key
FT	Active-site
XX	Location/Qualifiers
XX	102..106
PN	WO200028047-A1.
XX	
XX	18-MAY-2000.
PD	
XX	
PF	29-OCT-1999; 99WO-US25523.
XX	
PR	06-NOV-1998; 98US-0187789.
XX	
XX	(UYJE-) UNIV JEFFERSON THOMAS.
PA	
XX	
XX	Alnemri ES, Fernandez-Alnemri T;
PI	
XX	
DR	WPI; 2000-376558/32.
DR	N-PSDB; AAA15166.
PT	Novel nucleic acids encoding cell death specific protease termed
XX	caspase-14 useful for treating cancers by stimulating apoptosis -
XX	
PS	Claim 42; Fig 9; 78pp; English.
XX	
CC	The present sequence represents a human caspase-14 splice variant. The
CC	polypeptide is a cell death specific protease, and is an apoptosis
CC	stimulator. Caspase-14 polynucleotides and polypeptides, and
CC	anti-caspase-14 antibodies are useful for treating or reducing the
CC	severity of pathological conditions associated with increased or
CC	decreased levels of apoptosis. Apoptosis mediated diseases such as

CC AIDS, neurodegenerative diseases and ischemic injury are treated by  
 CC administering anti-caspase-14 antibodies. The antibody is useful for  
 CC determining the presence or the level of caspase-14 in tissue sample  
 CC and also for the isolation of caspase-14 with apoptotic activity or  
 CC in screening assay to identify an agent that inhibits heterodimer or  
 CC heterotrimer formation and therefore, apoptosis.

XX Sequence 214 AA;

Query Match 59.6%; Score 804.5; DB 21; Length 214;  
 Best Local Similarity 63.0%; Pred. No. 2.3e-74; Indels 41; Gaps 3;  
 Matches 160; Conservative 27; Mismatches 26;

QY 8 MSDDPQIPEERYDMSGARLALTLCTVKAREGSEVDMLERMFYLFKESTMKRDPPTAQ 67  
 Db 1 MSNRSLEEEKYDMSGARLALTLCTVKAREGSE----- 34  
 QY 68 FLEELDFEQITIDWEEBPVSCAFVVLMAHGEGLKGEDEKMYRLJDLFEVLNNKNCAL 127  
 Db 35 --EELEKFOQAIDSRDEDPVSCAFVVLMAHGEGLKGEDEKMYRLJDLFEVLNNKNCAL 92  
 QY 128 RGRKRVYIIQACRGEHRDPGEBELRGNEELGDEELGDE--VAVLKNNPOSIPYTDLTH 186  
 Db 93 RAKPRVYIIQACRGEHRDPG-----ETVGDDEIYMWIKDSPQITPTTDALHV 140  
 QY 187 YSTVEGYLSYRHDEKSGSFIOTLDVFIHKGSILELTEITRLMANTENVQEGKPRKN 246  
 Db 141 YSTVEGYLAHNDQKSGFIOTLDVFIHKGHILELLETVTRMAELVQEGKARNTN 200  
 QY 247 PEVOSTLRKRLYLQ 260  
 Db 201 PEIOTLRKRLYLQ 214

RESULT 9  
 AAY93215

ID AAY93215 standard; Protein; 230 AA.

XX AC AAY93215;

XX DT 04-SEP-2000 (first entry)

XX DE Amino acid sequence of a human caspase-14 splice variant.

XX KW Caspase-14; cell death specific protease; apoptosis stimulator;  
 KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Active-site 130..134

XX PN WO200028047-A1.

XX PD 18-MAY-2000.

XX PF 29-OCT-1999; 99WO-US25523.

XX PR 06-NOV-1998; 98US-0187789.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES, Fernandez-Alnemri T;

XX DR WPI; 2000-376558/32.

XX DR N-PSDB; AAA15165.

XX PT Novel nucleic acids encoding cell death specific protease termed  
 PT caspase-14 useful for treating cancers by stimulating apoptosis

XX PS Claim 41; Fig 8; 78pp; English.

XX CC The present sequence represents a human caspase-14 splice variant. The

CC polypeptide is a cell death specific protease, and is an apoptosis  
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and  
 CC anti-caspase-14 antibodies are useful for treating or reducing the  
 CC severity of pathological conditions associated with increased or  
 CC decreased levels of apoptosis. Apoptosis mediated diseases such as  
 CC AIDS, neurodegenerative diseases and ischemic injury are treated by  
 CC administering anti-caspase-14 antibodies. The antibody is useful for  
 CC determining the presence or the level of caspase-14 in tissue sample  
 CC and also for the isolation of caspase-14 with apoptotic activity or  
 CC in screening assay to identify an agent that inhibits heterodimer or  
 CC heterotrimer formation and therefore, apoptosis.

XX Sequence 230 AA;

Query Match 51.3%; Score 692.5; DB 21; Length 230;  
 Best Local Similarity 72.0%; Pred. No. 8.7e-63;  
 Matches 134; Conservative 22; Mismatches 17; Indels 13; Gaps 2;

QY 8 MSDDPQIPEERYDMSGARLALTLCTVKAREGSEVDMLERMFYLFKESTMKRDPPTAQ 67  
 Db 1 MSNRSLEEEKYDMSGARLALTLCTVKAREGSEBDLALHMFQRLFESTMKRDPPTAQ 60  
 QY 68 FLEELDFEQITIDWEEBPVSCAFVVLMAHGEGLKGEDEKMYRLJDLFEVLNNKNCAL 127  
 Db 61 FOEBLEKFOQAIDSRDEDPVSCAFVVLMAHGEGLKGEDEKMYRLJDLFEVLNNKNCAL 120  
 QY 128 RGRKRVYIIQACRGEHRDPGEBELRGNEELGDEELGDE--VAVLKNNPOSIPYTDLTH 186  
 Db 121 RAKPRVYIIQACRGEHRDPG-----ETVGDDEIYMWIKDSPQITPTTDALHV 168  
 QY 187 YSTVEG 192  
 Db 169 YSTVEG 174

RESULT 10  
 AAU72882

ID AAU72882 standard; Protein; 234 AA.

XX AC AAU72882;

XX DT 26-FEB-2002 (first entry)

XX DE Human aspartyl protease partial protein sequence #7.

XX KW Human; protease; PCR primer; cytosolic; immunomodulator; cardiant;  
 KW vasotrophic; antimigraine; analgesic; endocrine; nootropic; tranquilizer;  
 KW hypertensive; neuroleptic; neuroprotective; anabolic;  
 KW anorectic; antiinflammatory; aspartyl protease; cysteine protease;  
 KW metalloprotease; serine protease; cancer; haematopoietic; breast; colon;  
 KW lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;  
 KW immune-related disease; cardiovascular disease; neuronal disease;  
 KW migraine; sexual dysfunction; mood disorder; attention disorder;  
 KW cognition disorder; hypotension; hypertension; psychotic disorder;  
 KW dyskenesia; metabolic disorder; inflammatory disorder.

XX OS Homo sapiens.

XX PN WO200183782-A2.

XX PD 08-NOV-2001.

XX PF 04-MAY-2001; 2001WO-US14431.

XX PR 04-MAY-2000; 2000US-201879P.

XX PA (SUGEN-) SUGEN INC.

XX PI Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;

XX PI Payne V;

XX DR WPI; 2002-041502/05.

XX DR N-PSDB; AAS97165.

XX Novel protease polypeptide useful for screening for substances that may  
PT be used to treat, e.g., cancers, immune-related diseases,  
PT cardiovascular disease, migraine, pain, psychotic and inflammatory  
PT disorders -  
XX  
PS Claim 28, Figure 2A; 232pp; English.  
XX  
CC The invention relates to an isolated, enriched, or purified protease  
CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to  
CC screen for substances (S) that may modulate its activity. Administering  
CC S (which modulates protease activity in vitro) may be used to treat a  
CC disease or disorder selected from cancers (e.g., of tissues, of blood or  
CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,  
CC brain, ovarian, bladder or kidney), immune-related diseases and  
CC disorders, cardiovascular disease, brain or neuronal-associated diseases  
CC (e.g., central or peripheral nervous system diseases, migraine, pain,  
CC sexual dysfunction, mood disorders, attention disorders, cognition  
CC disorders, hypotension, hypertension, psychotic disorders, neurological  
CC disorders and dyskinesias), metabolic disorders and inflammatory  
CC disorders. (I) may also be useful as a diagnostic tool for a disease or  
CC disorder such as those above. AAU72876-AAU72910 represent human  
CC protease amino acid sequences of the invention.  
XX  
SQ Sequence 234 AA;  
  
Query Match 31.6%; Score 427; DB 23; Length 234;  
Best Local Similarity 39.7%; Pred. No. 1.9e-35;  
Matches 102; Conservative 45; Mismatches 72; Indels 38; Gaps 7;  
  
QY 18 RYDMSGARLALTLCTVARESGEVDMEALERMFRYLKFESTMKDPPTAQOFLBELDEFOQ 77  
Db 1 QYDLSKARALLLVIGICRPGAOHDVEALGICWALGFETTRDPTAQARQELAQPRE 60  
QY 78 TIDNMEPVCACFVPLMAH-GEELKGEDEKMYRLDELFLVANNKCKALRGKPKYIT 136  
Db 61 QLTICRGPVSCALVALMAHGGPRQLGADQEQVPELMQELS--RQVVIQGRPKIFLL 118  
QY 137 QACRGEHRDGG-----ELRGNBELGDEBELGDEVAVLKNNPOSIPYTDTLHI 186  
Db 119 QACRGRNDGAVGPTALPWYMSWLR-----PPSVSHADVIQI 157  
QY 187 YSTVEGYLSYRHDEKSGFIQTLTDVFIHKKG-SILELTEBITRLMANTVMOE--GKPR 243  
Db 158 YAAQGVAVAR-DDKSGDFIQTIVELVRANPGRDLLELTVNVRVCEQEVLPDCCBLR 216  
QY 244 KVMDEVOSTLRKLYLQ 260  
Db 217 KACLEIRSRRLRLCLQ 233  
  
RESULT 11  
AAE00610  
ID AAE00610 standard; Protein; 261 AA.  
XX  
AC AAE00610;  
XX  
DT 02-JUL-2001 (first entry)  
XX  
DE Chimeric cassette comprising human caspase with modified cleavage site.  
XX  
KM Human: caspase; beta-secretase; cleavage site; interdomain linker;  
KM cysteine protease; apoptosis; caspase expression cassette; metastasis;  
KM tumour; cathepsin B; urokinase; proliferation; gene therapy; chimera;  
KM Alzheimer's disease.  
XX  
OS Chimeric - Homo sapiens.  
OS Chimeric - Unidentified.  
FH  
FT Key Location/Qualifiers  
FT Region 1..147  
FT 148..165  
FT Region

FT /note= "beta-secretase cleavage site which replaces  
FT the naturally occurring caspase cleavage site"  
FT Region 166..261  
FT /label= Caspase\_small\_subunit  
XX  
PN WO200129232-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 19-OCT-2000; 2000MO-US28941.  
XX  
PR 20-OCT-1999; 99US-0160559.  
XX  
PR 14-AUG-2000; 2000US-0225564.  
XX  
PA (SCIO-) SCIOS INC.  
XX  
PI Cordell B, Li Y;  
XX  
PI WPI; 2001-290920/30.  
DR N-PSDB; AAD03918.  
XX  
PT Novel fusion polypeptide comprising first and second caspase subunit  
PT separated by cleavage site not associated in nature with caspase  
PT subunit, useful for cloning gene encoding enzymes involved in  
PT proteolytic cleavage -  
XX  
PS Example 1; Fig 27; 116pp; English.  
XX  
CC The present amino acid sequence is an artificially engineered chimeric  
CC cassette construct comprising human caspase-3 with interdomain linker  
CC replaced by a swedish mutant beta-secretase cleavage site. This modified  
CC caspase-3 plays a pivotal role in Alzheimer's disease. Caspases are  
CC a family of cysteine proteases, that participate in the initiation and  
CC execution of apoptosis. Caspases exist as pro-enzymes, activated by  
CC cleavage into a large and small subunit, occurring after specific  
CC aspartic acid residues within the pro-enzyme sequence.  
CC The present invention relates to a method for functional cloning of genes  
CC encoding proteins or enzymes involved in proteolytic cleavage. The  
CC invention is based on the use of caspase expression cassettes comprising  
CC the coding sequence of a proteolytic cleavage site flanked by sequences  
CC encoding two caspase subunit. A fusion polypeptide comprising a first  
CC and a second caspase subunit, separated by a cleavage site not associated  
CC in nature, is useful for cloning gene encoding enzymes involved in  
CC proteolytic cleavage. An expression cassette containing fusion  
CC polypeptide is used to identify a mutant cell line deficient in an  
CC enzyme of interest and is also useful for diagnosis and suppression of  
CC proliferation or metastases of a tumour cell characterised by  
CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,  
CC selectively expressed in the tumour cells). DNA encoding fusion  
CC polypeptide is used in gene therapy.  
XX  
SQ Sequence 261 AA;  
  
Query Match 21.2%; Score 286.5; DB 22; Length 261;  
Best Local Similarity 32.1%; Pred. No. 6.4e-21;  
Matches 85; Conservative 41; Mismatches 104; Indels 35; Gaps 9;  
  
QY 16 EERYDMSGARLALTLCTV-----AREGSEVDMEALERMFRYLKFESTMKDPPTA 65  
Db 7 DNYSKMDYPEWGLCIILINNKFHKSTGMTSGTGDVDAANIRFTRMLKYEVRRKNDLTR 66  
QY 66 QQFLBELDEFOQTLIDNMEPVCACFV-VLMAHGEELKGEDEGMVLEDFEVLANNKNC 124  
Db 67 ---EBIVELMRDYSKSDHSKRSSFVCLVLSHGEGEILFGNGP-VDUKKTINFRGDR 121  
QY 125 KALRGKPRVYIIQACRGEHRDPGEELRGN--ELGDEBELGDEVAVLKNNPOSIPYTD 182  
Db 122 RSLRGKPRKFLIIQACRGTBELDGGIETKTEISEVNLDAEPHDSMACHK-----IPY 176  
QY 183 TLHISTVEGYLSYRHDEKSGFIQTLTDVFIHKKG-SILELTEBITRLMANTVMOE--GK 241  
Db 177 FLVAYSTAPGYYSWRNSKDSWFIQSLC-AMLKQYADKLEPMHILTRV--NRKVAITEFS 233

QY 242 -----PRKVPNEVOSTLRKKLY 258  
 Db 234 FSPDATHAKQIPCIYVSMLTRKELY 258

RESULT 12  
 ID ABB10110 standard; Protein; 452 AA.

XX ABB10110;

XX 26-JUL-2002 (first entry)

XX Mouse caspase 2 protein.

XX Caspase 2; antitense; cytosstatic; osteopathic; cerebroprotective;  
 KW neuroprotective; antilipemic; antinflammatory; antimicrobial;  
 KW haematopoietic disorder; bone metabolism disorder; cholesterol disorder;  
 KW hyperproliferative disorder; cancer; blood disorder; stroke;  
 KW brain injury; neurodegenerative disease; infection; inflammation;  
 KW tumour.

XX Mus musculus.

XX WO200224720-A1.

XX 28-MAR-2002.

XX 14-SEP-2001; 2001WO-US28631.

XX 20-SEP-2000; 2000US-0667018.

XX (ISIS-) ISIS PHARM INC.

XX Zhang H, Watt AT;

XX WPI; 2002-351998/38.

XX N-PSDB; ABB58563.

PT New antisense compounds targeted to nucleic acid molecule encoding  
 PT caspase 2, useful for treating diseases or conditions associated with  
 PT caspase 2, e.g. cancer, blood disorders, stroke, brain injury and  
 PT neurodegenerative diseases -  
 XX Example 13; Page 111-113; 146pp; English.

XX The invention relates to a compound 8-50 nucleobases in length targeted  
 CC to a nucleic acid molecule encoding caspase 2, which specifically  
 CC hybridises with and inhibits the expression of caspase 2, or specifically  
 CC hybridises with at least an 8-nucleobase portion of an active site on a  
 CC nucleic acid molecule encoding caspase 2. The activity of antisense  
 CC oligonucleotides of the invention may be described as, cytosstatic,  
 CC osteopathic, cerebroprotective, neuroprotective, antilipemic,  
 CC antiinflammatory and antimicrobial. The antisense compounds are useful  
 CC for treating an animal having a disease or condition associated with  
 CC caspase 2, such as haematopoietic disorder, bone metabolism disorder,  
 CC cholesterol disorder, or a hyperproliferative disorder. These compounds  
 CC may further be used as research reagents and diagnostics, to distinguish  
 CC between functions of various members of a biological pathway, in the  
 CC treatment of a disease or disorder which can be treated by modulating  
 CC the expression of caspase 2, including cancer, blood disorders,  
 CC stroke, brain injury and neurodegenerative diseases. They may also be  
 CC used for prophylaxis, e.g. to prevent or delay infection, inflammation or  
 CC tumour formation. The current sequence represents the mouse caspase 2  
 CC protein.

XX Sequence 452 AA;

Query Match 20.5%; Score 276.5; DB 23; Length 452;

Best Local Similarity 30.6%; Pred. No. 1.6e-19; Indels 13; Gaps 6;  
 Matches 71; Conservative 53; Mismatches 95;

QY 36 REGSEVDMALERMFRYLKFESTMKRDPPTAQOFLBELDEFQOTIDNMEEPVSCAFVUMA 95

Db 219 RSGDGVHTTLVTLFKLGVNVAHLDQTAQEMQKQNFQAQ-IPAIRVYDSCV-VALLS 276  
 QY 96 HGEELKKGDEKMWRLLEDLFEVLNNKNCALRGKPRVY11OACRGHRDPG---EELRG 152  
 Db 277 HGVGGYGVNDGKLLQLOEVRLLFDNANCPSLONKPMFLLQACRGDETBGVDQDQGN 336  
 QY 153 NEELGGDEELGGDEVAVKNNPQSIPTVYDTLHYSVVEGYLSYRHDEKSGF1QTLTDV 212  
 Db 337 HTQSPGCEESDAGKEBLMK--MRLPTRSDM1CGYACILKGNAMRNTKRGSGWYIEALTQV 393  
 QY 213 F1HKKG--1LELTETRLMANTENWQEGK---RKNPEVOSTLRKKLYL 259  
 Db 394 FSRACDMHVAADMLVKVVALIKEREGYAPGTEFHRCKEMSEYCS1LCOQLYL 445

RESULT 13  
 ID AAU05395 standard; Protein; 277 AA.

XX AAU05395;

XX 24-OCT-2001 (first entry)

XX Mouse caspase 3.

XX Mouse; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;  
 KW viral infection; haematopoietic disorder; autoimmune disorder;  
 KW atherosclerosis; neurological disorder.

XX Mus musculus.

XX WO200153310-A1.

XX 26-JUL-2001.

XX 11-JAN-2001; 2001WO-US00888.

XX 18-JAN-2000; 2000US-0484617.

XX (ISIS-) ISIS PHARM INC.

XX Zhang H, Cowsett LM;

XX WPI; 2001-442252/47.

XX N-PSDB; AAS10510.

PT New antisense compound to inhibit caspase 3 is useful for treating  
 PT hepatitis and atherosclerosis -  
 XX Disclosure; Page 96-97; 127pp; English.

XX The present sequence representing mouse caspase 3 is described  
 CC in an invention relating to novel antisense oligonucleotides  
 CC (AAS10517-AAS10676) and methods of using these compounds for the  
 CC modulation of caspase 3 expression. The caspase 3 antisense  
 CC oligonucleotides specifically hybridise with and inhibit the  
 CC expression of caspase 3. Antisense compounds targeted to caspase 3  
 CC are useful to inhibit caspase 3 expression in cells or tissues and  
 CC to modulate apoptosis. The caspase 3 antisense oligonucleotides are  
 CC useful for treating disorders associated with expression of caspase 3.  
 CC Such disorders include hyperproliferative disorders (e.g. cancer),  
 CC viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune  
 CC disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's  
 CC disease).

XX Sequence 277 AA;

Query Match 20.4%; Score 276; DB 22; Length 277;

Best Local Similarity 33.3%; Pred. No. 8.4e-20; Indels 38; Gaps 9;  
 Matches 79; Conservative 39; Mismatches 81;

QY 35 AREGSEVDMALERMFRYLKFESTMKRDPPTAQOFLBELDEFQOTIDNMEEPVSCAFV-VL 93

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Db 63 SRSGTVDANLLETFEGLYVQVANKNDLTREDLLEMD-----SVSKEDSKRSFPCV 118
Qy 94 MARGESGLKGEDEKAVRLLEDLFEVLNNKNCALRGKPKVYIIQA CRGHRDPGEELRGNE 153
Db 119 LSHGDEGVIVGTNGP-VELKKLTGFFRGDYCRSLTGKPKFIIOACGTGLDGCIF---- 173
Qy 154 EELGDEELGDEVAVLKKNPQSIPTVDTLHITVSGYLSYRHDEKSGGFIQTLD-- 211
Db 174 TDSGTDEEMA-----CQKIPVADFLVAYSTA PGYYSMNRSKDSWFIQSLCML 223
Qy 212 -VTHKKGSLLELTETRLMANTENVQEGK-----PRKVPVQSTLRKKLY 258
Db 224 KLYAHK---LEFMHILTRV--NRKVATEFESFSLDSTFPAKKOIPCIVSMLTRELY 274

RESULT 14
AAR90703
ID AAR90703 standard; Protein; 435 AA.
AC AAR90703;
XX
XX 10-APR-1996 (first entry)
DT
DE Interleukin-1-beta converting enzyme like apoptosis protease-2.
XX
XX Interleukin-1-beta converting enzyme like apoptosis protease-2;
XX ICE-LAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;
XX Parkinson disease; septic shock; rheumatoid arthritis; head injury;
XX antitumor; antiviral.
XX Homo sapiens.
XX MO9600297-A1.
XX
XX 04-JAN-1996.
XX
XX 23-JUN-1994; 94WO-US07127.
XX
XX 23-JUN-1994; 94WO-US07127.
XX
XX 23-JUN-1994; 94WO-US07127.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Craig AR, Haeflins GA, Hudson PL, Kirkness EF, Wei WH;
XX
XX WPI: 1996-068881/07.
XX
XX N-PSDB; AAT15579.
XX
XX Interleukin-1 beta converting enzyme like apoptosis protease-1 and
XX PT - controls programmed cell death, used in treatment of
XX PT immunosuppression related disorders, e.g. AIDS and Alzheimer's
XX PT disease
XX
XX Claim 1; Fig 2A-C; 58pp; English.
XX
XX Human interleukin-1-beta converting enzyme like apoptosis protease-2
XX CC (ICE-LAP-2) (AAR90703) is structurally related interleukin-1-beta
XX CC converting enzyme, which is responsible for apoptosis. Recombinant
XX CC ICE-LAP-2 is obd. by expression of encoding cDNA (AAT15579) in
XX CC prokaryotic or eucaryotic host cells. It is used to treat diseases
XX CC related to abnormally controlled programmed cell death, to control
XX CC vertebrate development and tissue homeostasis, to overcome viral
XX CC infections and to treat immunosuppression-related disorders.
XX
XX Sequence 435 AA;
SO

Query Match 20.4%; Score 275.5; DB 17; Length 435;
Best Local Similarity 29.6%; Pred. No. 1.9e-19;
Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;
Qy 36 RESSEVDMLEMFRLKPESTMKRDPITAOQFLBELEDFQOITIDNMBEVSQAFVITMA 95
Db 202 RSGGDVDSHTLVTLFKLLGYDVHVLCDOTAQEMOEKLFNPAO-LPAHRTVDSQ-IVALLS 259

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Qy 96 HGEGLKGEDEKAVRLLEDLFEVLNNKNCALRGKPKVYIIQA CRGHRDPGEELRGNE 155
Db 260 HGVGALYGVDAKLLQAEVFOGFDNANCPSLQNKPKMFMFIQA CRGDETRGVDDQDGKN 319
Qy 156 LGGDEELGDEVAVLKKNPQSIPTVDTLHITVSGYLSYRHDEKSGGFIQTLDVFIH 215
Db 320 HAQSPGCEESDACKEXLPKVRLPTSPDMICGACLKGTAMRYTKRGSWYIEALQVF-S 378
Qy 216 KKGSLLELTETRLMANTENVQEGKPR-----KNVPEVQSTLRKKLY 259
Db 379 ERGDMHVAIDLKVALIKDRGVAPGTEFHRCKENSEVCSLTCRHL 428

RESULT 15
AAR66771
ID AAR66771 standard; Protein; 435 AA.
AC AAR66771;
XX
XX 13-SEP-1995 (first entry)
DT
DE Human interleukin-1 beta converting enzyme ced 3 homolog Ich-1(L).
XX
XX Human interleukin-1 beta converting enzyme ced 3 homolog; Ich-1(L);
XX KM oncogene bcl-2; programmed cell death; cancer treatment.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Active-site 301..305
XX
XX MO9500160-A.
XX
XX 05-JAN-1995.
XX
XX 10-JUN-1994; 94WO-US06630.
XX
XX 24-JUN-1993; 93US-0080850.
XX
XX (GCHO) GEN HOSPITAL CORP.
XX
XX Miura M, Yuan J;
XX
XX WPI: 1995-051742/07.
XX
XX N-PSDB; AAO79971.
XX
XX Promoting or preventing programmed cell death in vertebrate cells
XX PT - by inhibiting the activity of interleukin-1 beta converting
XX PT enzyme.
XX
XX Example 5; Fig 12A; 116pp; English.
XX
XX AAO79971 encodes AAR66771 human interleukin-1 beta converting enzyme
XX CC ced 3 homolog Ich-1(L), increasing Ich-1(L)'s enzymatic activity can
XX CC promote the programmed cell death of cancer cells (pref. those
XX CC overexpressing the bcl-2 oncogene), this can be used as the basis
XX CC of a new cancer treatment. Alternatively by reducing Ich-1(L)'s
XX CC enzymatic activity programmed cell death can be inhibited, this may
XX CC be useful in the development of new cell lines which remain viable in
XX CC culture for extended or indefinite periods, independant of growth
XX CC factors.
XX
XX Sequence 435 AA;
SO

Query Match 20.3%; Score 274.5; DB 16; Length 435;
Best Local Similarity 29.7%; Pred. No. 2.4e-19;
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;
Qy 36 RESSEVDMLEMFRLKPESTMKRDPITAOQFLBELEDFQOITIDNMBEVSQAFVITMA 95
Db 202 RSGGDVDSHTLVTLFKLLGYDVHVLCDOTAQEMOEKLFNPAO-LPAHRTVDSQ-IVALLS 259

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Oy 96 HGEGLKGBEBKXVRLJEDLEFVNLNNKSKALRQKPKYU11QACRGHNRPGELKGNEE 155
Db 260 HGVEBAL1GVGVGKLLQLEDEVFOLRPNNAKPSLQNKPKFF1QACRGSETRGVDOQGN 319
Oy 156 LGGDEBLGGDEAVLKNPNOS1PFYUPTRL1HY5VVEGYL5YRHEKSGCE1OTLTDF1H 215
Db 320 HAGSGGCEESDAGKEKLPKMRLLPFRSDM1CGYACLKGTAAANRN1KRSW1TEALAQVFE 379
Oy 216 KKG5--1LELTETETRLMANTENVMOGKP--RKVNEVOSTLTKKLYL 259
Db 380 RACDMHNVADMLKVNALIKDBEGVAPGTEFNRKCEMSYGCSTLGRHLYL 428

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OM protein - protein search, using sw model

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(without alignments)  
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Title: US-09-989-903-2

Perfect score: 1350  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1350	100.0	260	US-09-187-789-2	Sequence 2, Appl
2	1350	100.0	260	US-09-139-600-2	Sequence 2, Appl
3	934.5	69.2	242	US-09-187-789-5	Sequence 5, Appl
4	804.5	59.6	214	US-09-187-789-9	Sequence 9, Appl
5	692.5	51.3	230	US-09-187-789-7	Sequence 7, Appl
6	384	28.4	74	US-09-187-789-63	Sequence 63, Appl
7	384	28.4	74	US-09-187-789-63	Sequence 63, Appl
8	299	22.1	56	US-09-187-789-64	Sequence 58, Appl
9	299	22.1	56	US-09-187-789-64	Sequence 64, Appl
10	280	20.7	53	US-09-139-600-59	Sequence 59, Appl
11	280	20.7	53	US-09-139-600-60	Sequence 59, Appl
12	275.5	20.4	435	PCT-US94-07127A-4	Sequence 60, Appl
13	274.5	20.3	421	US-08-963-502-10	Sequence 10, Appl
14	274.5	20.3	421	US-08-963-502-10	Sequence 10, Appl
15	274.5	20.3	435	PCT-US96-10521-10	Sequence 10, Appl
16	274.5	20.3	435	US-08-258-287B-53	Sequence 53, Appl
17	274.5	20.3	435	US-08-368-704C-51	Sequence 51, Appl
18	274.5	20.3	435	US-09-561-756-9	Sequence 9, Appl
19	274.5	20.3	435	US-09-227-721-9	Sequence 9, Appl
20	274.5	20.3	441	US-08-816-075-2	Sequence 2, Appl
21	274.5	20.3	441	US-08-258-287B-44	Sequence 44, Appl
22	274.5	20.3	441	US-08-368-704C-43	Sequence 43, Appl
23	274.5	20.3	277	US-08-890-542A-2	Sequence 2, Appl
24	274.5	20.3	277	US-08-591-605-2	Sequence 2, Appl
25	274.5	20.3	277	US-08-964-308-6	Sequence 6, Appl
26	274.5	20.3	277	US-08-462-969B-4	Sequence 4, Appl
27	274.5	20.3	277	US-08-964-313-6	Sequence 6, Appl

28	273	20.2	277	4	US-09-561-756-12	Sequence 12, Appl
29	273	20.2	277	4	US-09-227-721-12	Sequence 10, Appl
30	273	20.2	277	4	US-08-983-502-30	Sequence 30, Appl
31	273	20.2	277	5	PCT-US96-10521-30	Sequence 30, Appl
32	265	19.6	503	3	US-08-258-287B-36	Sequence 36, Appl
33	265	19.6	503	3	US-08-368-704C-36	Sequence 36, Appl
34	264	19.6	277	3	US-08-964-313-10	Sequence 10, Appl
35	264	19.6	277	3	US-08-964-313-10	Sequence 10, Appl
36	264	19.6	277	4	US-09-069-138-10	Sequence 37, Appl
37	263.5	19.5	497	3	US-08-368-704C-37	Sequence 37, Appl
38	263.5	19.5	497	3	US-08-368-704C-37	Sequence 37, Appl
39	259	19.2	505	2	US-08-394-189B-5	Sequence 5, Appl
40	259	19.2	505	5	PCT-US93-05701-20	Sequence 5, Appl
41	259	19.2	505	5	PCT-US93-05705-5	Sequence 5, Appl
42	255.5	18.9	303	4	US-09-561-756-24	Sequence 24, Appl
43	255.5	18.9	303	4	US-09-227-721-24	Sequence 24, Appl
44	255.5	18.9	303	4	US-08-556-627A-2	Sequence 2, Appl
45	253	18.7	416	3	US-08-852-936C-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-187-789-2  
Sequence 2, Application US/09187789.  
Patent No. 6340740  
GENERAL INFORMATION:  
APPLICANT: Altemet, Emad S.  
APPLICANT: Fernandez-Altemet, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
FILE REFERENCE: 480140.434C1  
CURRENT APPLICATION NUMBER: US/09/187, 789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-187-789-2

Query Match 100.0%; Score 1350; DB 4; Length 260;  
Best Local Similarity 100.0%; Pred. No. 5.6e-135;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPDMESEMSDPPQLOERYDMSGARLALTLCTKAREGEVDMELERFYLKFESTMK 60  
D 1 KPDMESEMSDPPQLOERYDMSGARLALTLCTKAREGEVDMELERFYLKFESTMK 60

QY 61 RDPTRNOQFLERLDFEFOOTIDMWEPPVSCAFVLMANHEEGILKGEDEDMVRLDELFEVLN 120  
D 61 RDPTRNOQFLERLDFEFOOTIDMWEPPVSCAFVLMANHEEGILKGEDEDMVRLDELFEVLN 120

QY 121 NKNCKALRGKRVKVIIOACRGEHRDPGBELRGNEELGDEELGDEVAVLKNNPOSIPITY 180  
D 121 NKNCKALRGKRVKVIIOACRGEHRDPGBELRGNEELGDEELGDEVAVLKNNPOSIPITY 180

QY 181 TDTLHIVSYVGVLSYRHDGSGFIOTLDVFIHKKSIIELTEITRLMANTVMEQ 240  
D 181 TDTLHIVSYVGVLSYRHDGSGFIOTLDVFIHKKSIIELTEITRLMANTVMEQ 240

QY 241 KPRKNPEVOSTLRKKLYLQ 260  
D 241 KPRKNPEVOSTLRKKLYLQ 260

RESULT 2  
US-09-139-600-2  
Sequence 2, Application US/09139600  
Patent No. 6432628  
GENERAL INFORMATION:

```
APPLICANT: Alnemri, Emdad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHOD OF USE
FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139.600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 260
TYPE: PRT
ORGANISM: Mus musculus
US-09-139-600-2
```

```
Query Match          100.0%; Score 1350; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 5.6e-135;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KPDSEMSDPOLOEERYDMSGARLALTLCVTKAREGSEVDMALERMFRYLKESTWK 60
Db 1 KPDSEMSDPOLOEERYDMSGARLALTLCVTKAREGSEVDMALERMFRYLKESTWK 60
Qy 61 RDPTRQOFLIEIDFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKAVRLLEDLFEVLN 120
Db 61 RDPTRQOFLIEIDFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKAVRLLEDLFEVLN 120
Qy 121 MNCKALGKPKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 180
Db 121 MNCKALGKPKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 180
Qy 181 TDLTHIVSTVEGYLSYRDEKSGFIQTLTDVFIHKKSILLETITRLMANTVMOEG 240
Db 181 TDLTHIVSTVEGYLSYRDEKSGFIQTLTDVFIHKKSILLETITRLMANTVMOEG 240
Qy 241 KPRKVNPEVOSTLRKKLYLQ 260
Db 241 KPRKVNPEVOSTLRKKLYLQ 260
```

```
RESULT 3
US-09-187-789-5
Sequence 5, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emdad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187.789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-5
```

```
Query Match          69.2%; Score 934.5; DB 4; Length 242;
Best Local Similarity 70.9%; Pred. No. 5.2e-91;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
```

```
Qy 8 MSDPPOLOEERYDMSGARLALTLCVTKAREGSEVDMALERMFRYLKESTWK 67
Db 1 MSNPRLSEBEKYMDSGARLALTLCVTKAREGSEVDMALERMFRYLKESTWK 60
Qy 68 FLEELDEFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKAVRLLEDLFEVLN 127
Db 61 FOEELKEFQOALDSREDPVSCAFVVLMAHGEGLKGEDEKAVRLLEDLFEVLN 120
Qy 128 RGPVKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 186
```

```
Db 121 RAKPKVYIIQACRGHRDGP-----ETVGGDEIVWVINDSPQITPTYTDALHV 168
Qy 167 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKSILLETITRLMANTVMOEGKPRKVN 246
Db 169 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKSILLETITRLMANTVMOEGKPRKVN 228
Qy 247 PEVOSTLRKKLYLQ 260
Db 229 PEVOSTLRKKLYLQ 242
```

```
RESULT 4
US-09-187-789-9
Sequence 9, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emdad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187.789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-9
```

```
Query Match          59.6%; Score 804.5; DB 4; Length 214;
Best Local Similarity 63.0%; Pred. No. 2.6e-77;
Matches 160; Conservative 27; Mismatches 26; Indels 41; Gaps 3;
```

```
Qy 8 MSDPPOLOEERYDMSGARLALTLCVTKAREGSEVDMALERMFRYLKESTWK 67
Db 1 MSNPRLSEBEKYMDSGARLALTLCVTKAREGSE----- 34
Qy 68 FLEELDEFQOITIDNMEEPVSCAFVVLMAHGEGLKGEDEKAVRLLEDLFEVLN 127
Db 35 --EELEKFOALDSREDPVSCAFVVLMAHGEGLKGEDEKAVRLLEDLFEVLN 92
Qy 128 RGPVKVYIIQACRGHRDGEELRGNEELGDEELGDEVANLKNPQISPT 186
Db 93 RAKPKVYIIQACRGHRDGP-----ETVGGDEIVWVINDSPQITPTYTDALHV 140
Qy 187 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKSILLETITRLMANTVMOEGKPRKVN 246
Db 141 YSTVEGYLSYRDEKSGFIQTLTDVFIHKKSILLETITRLMANTVMOEGKPRKVN 200
Qy 247 PEVOSTLRKKLYLQ 260
Db 201 PEVOSTLRKKLYLQ 214
```

```
RESULT 5
US-09-187-789-7
Sequence 7, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemri, Emdad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187.789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 230
```



TYPE: PRT  
ORGANISM: Homo sapien  
US-09-187-789-7

Query Match 51.3%; Score 692.5; DB 4; Length 230;  
Best Local Similarity 72.0%; Pred. No. 2.1e-65;  
Matches 134; Conservative 22; Mismatches 17; Indels 13; Gaps 2;

QY 8 MSDDPQLQERBYDMSGARLALTCTKARAGSEVDMEALERFYLKFESTMKSDPTAAQ 67  
DB 1 MSNRSLEEEFYDMSGARLALTCTKARAGSEVDMEALERFYLKFESTMKSDPTAAQ 60  
QY 68 FLEELDEFQOTIDNMBEVPSCAFVILMAHGEGLLKGEDEKVRLEDFEVLNNKCKAL 127  
DB 61 FOEELERFOQALDRDPVSCAFVILMAHGEGLLKGEDEKVRLEDFEVLNNKCKAL 120  
QY 128 RGRKRYTIIQACRGEHDPGSELARGNELGDEELGDFE-VAVLKNPQSTPTTDTLHI 186  
DB 121 RAKRYTIIQACRGEHDPGSELARGNELGDEELGDFE-VAVLKNPQSTPTTDTLHI 168  
QY 187 YSTVEG 192  
DB 169 YSTVEG 174

RESULT 6  
US-09-187-789-63  
Sequence 63, Application US/09187789  
Patent No. 6340740  
GENERAL INFORMATION:  
APPLICANT: Alnemati, Emad S.  
APPLICANT: Fernandez-Alnemati, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHODS OF USE  
FILE REFERENCE: 480140.434CI  
CURRENT APPLICATION NUMBER: US/09/187,789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: Patentin Ver. 2.0  
SEO ID NO 63  
LENGTH: 74  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-187-789-63

Query Match 28.4%; Score 384; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 1.8e-33;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ARGESEVDMEALERFYLKFESTMKSDPTAAQFLEELDEFQOTIDNMBEVPSCAFVILM 94  
DB 1 ARGESEVDMEALERFYLKFESTMKSDPTAAQFLEELDEFQOTIDNMBEVPSCAFVILM 60  
QY 95 AHGEGLLKGEDEK 108  
DB 61 AHGEGLLKGEDEK 74  
RESULT 7  
US-09-139-600-58  
Sequence 58, Application US/09139600  
Patent No. 6432628  
GENERAL INFORMATION:  
APPLICANT: Alnemati, Emad S.  
APPLICANT: Fernandez-Alnemati, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHOD OF USE  
FILE REFERENCE: 480140.434  
CURRENT APPLICATION NUMBER: US/09/139,600  
CURRENT FILING DATE: 1998-08-25  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: Patentin Ver. 2.0  
SEO ID NO 58

LENGTH: 74  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-139-600-58

Query Match 28.4%; Score 384; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 1.8e-33;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ARGESEVDMEALERFYLKFESTMKSDPTAAQFLEELDEFQOTIDNMBEVPSCAFVILM 94  
DB 1 ARGESEVDMEALERFYLKFESTMKSDPTAAQFLEELDEFQOTIDNMBEVPSCAFVILM 60  
QY 95 AHGEGLLKGEDEK 108  
DB 61 AHGEGLLKGEDEK 74

RESULT 8  
US-09-187-789-64  
Sequence 64, Application US/09187789  
Patent No. 6340740  
GENERAL INFORMATION:  
APPLICANT: Alnemati, Emad S.  
APPLICANT: Fernandez-Alnemati, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHODS OF USE  
FILE REFERENCE: 480140.434CI  
CURRENT APPLICATION NUMBER: US/09/187,789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: Patentin Ver. 2.0  
SEO ID NO 64  
LENGTH: 56  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-187-789-64

Query Match 22.1%; Score 299; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.2e-24;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MVRLEDLFEVLNNKCKALRGKPRVYIIQACRGEHDPGSELARGNELGDEELGG 164  
DB 1 MVRLEDLFEVLNNKCKALRGKPRVYIIQACRGEHDPGSELARGNELGDEELGG 56

RESULT 9  
US-09-139-600-59  
Sequence 59, Application US/09139600  
Patent No. 6432628  
GENERAL INFORMATION:  
APPLICANT: Alnemati, Emad S.  
APPLICANT: Fernandez-Alnemati, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHOD OF USE  
FILE REFERENCE: 480140.434  
CURRENT APPLICATION NUMBER: US/09/139,600  
CURRENT FILING DATE: 1998-08-25  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: Patentin Ver. 2.0  
SEO ID NO 59  
LENGTH: 56  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-139-600-59

Query Match 22.1%; Score 299; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.2e-24;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 MVRLEDLFEVLNNKCKALRGKPRVYIIQACRGEHDPGSELARGNELGDEELGG 164  
DB 1 MVRLEDLFEVLNNKCKALRGKPRVYIIQACRGEHDPGSELARGNELGDEELGG 56

Db 1 MWLEDLFEVLNNKCKALRGKPKVYIIQACRGHERDGEELRGNEELGDELOG 56

# RESULT 10

US-09-187-789-65  
 ; Sequence 65, Application US/09187789  
 ; Patent No. 6340740  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emed S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
 ; FILE REFERENCE: 480140.434C1  
 ; CURRENT APPLICATION NUMBER: US/09/187,789  
 ; CURRENT FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 78  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 65  
 ; LENGTH: 53  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-187-789-65

Query Match 20.7%; Score 280; DB 4; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-22;  
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 165 DEVAVLKNNPQSIPTTDLTIHYSTVEGYLSYRHEKSGSFTQTLTDVFIHKK 217  
 Db 1 DEVAVLKNNPQSIPTTDLTIHYSTVEGYLSYRHEKSGSFTQTLTDVFIHKK 53

# RESULT 11

US-09-139-600-60  
 ; Sequence 60, Application US/09139600  
 ; Patent No. 6432628  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emed S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
 ; FILE REFERENCE: 480140.434  
 ; CURRENT APPLICATION NUMBER: US/09/139,600  
 ; CURRENT FILING DATE: 1998-08-25  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 60  
 ; LENGTH: 53  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-139-600-60

Query Match 20.7%; Score 280; DB 4; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-22;  
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 165 DEVAVLKNNPQSIPTTDLTIHYSTVEGYLSYRHEKSGSFTQTLTDVFIHKK 217  
 Db 1 DEVAVLKNNPQSIPTTDLTIHYSTVEGYLSYRHEKSGSFTQTLTDVFIHKK 53

# RESULT 12

PCT-US94-07127A-4  
 ; Sequence 4, Application PC/TUS9407127A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HE, ET AL.  
 ; TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, an  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ; ADDRESS: CECCHI, STEWART & OLSTEIN  
 ; STREET: 6 BECKER FARM ROAD  
 ; CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07127A

FILING DATE: submitted herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-184

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 435 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR 2

MOLECULE TYPE: PROTEIN

PCT-US94-07127A-4

Query Match 20.4%; Score 275.5; DB 5; Length 435;  
 Best Local Similarity 29.6%; Pred. No. 8.3e-21;  
 Matches 68; Conservative 53; Mismatches 100; Indels 9; Gaps 4;

Oy 36 REGSEVDMEALERNFRYKFEETMKRDPFAOQFLELDEFQOTIDNNEEPVSCAFVYIMA 95  
 Db 202 RSGGDVDSHTLVTFKFLGVDVHVLCDTAOEMOEKLFQNFQA-LPAHRTVDS-C-IVALLS 259  
 Oy 96 HGEELKGEDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGHERDGEELRGNEE 155  
 Db 260 HGEELKGEDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGHERDGEELRGNEE 319  
 Oy 156 LGDEBELGDEVAVLKNNPQSIPTTDLTIHYSTVEGYLSYRHEKSGSFTQTLTDVFIH 215  
 Db 320 HAGSPGCEESDAGKEKLPKMLPTSRSDMTCYACLCGTAAMRNKIRGSGWYIEALAQVF-S 378  
 Oy 216 KKGSLLEETETRLMANTEVMOEGKPR-----KVNPEVOSTLRKKLYL 259  
 Db 379 ERGCDMIVADMLVKVNALIKDEGVAPGTEPRCKEMSEYCSILCRHLYL 428

RESULT 13  
 US-08-963-502-10  
 ; Sequence 10, Application US/08963502  
 ; Patent No. 6399327

GENERAL INFORMATION:  
 APPLICANT: David WALLACH  
 APPLICANT: Mark P. BOLDIN  
 APPLICANT: Tanya M. GONCHAROV  
 APPLICANT: Yuri V. GOLTSER  
 TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF PAS RECEPTORS  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Broadway and Neimark  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk



FILING DATE: 10-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/080,850  
FILING DATE: 24-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 0609,3920001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
TELEX: 248636 SSK  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 435 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-258-287B-53

Query Match 20.3%; Score 274.5; DB 3; Length 435;  
Best Local Similarity 29.7%; Pred. No. 1.1e-20;  
Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;  
QY 36 REGSEVDMEALERMFRYLKFEISTMKRDPTAQQFLELDPEFOOTIDNWEPEVSCAFVILMA 95  
DB 202 RSGGVDVHSTLVTLFKLGYDVHVLCDOTAQEMOEKLNFAQ-LPAHRTDSC-IVALLS 259  
QY 96 HGEGLKGEDEKAVRLLEDLEVLNNKCKALRGKPKVYIIQACGEHRDPGEELRGNEE 155  
DB 260 HVEGAIYGVGDKLQLQDEVFQLPDNANCPSLQNKPKMFFIOACRGDETDRCGVDOODGKN 319  
QY 156 LCGDEELGDEVAVALKNNPQSIPTYTDLHIYSTVEGYLSVRHDEKSGSEIQLTDVFIH 215  
DB 320 HAGSPGCEESDGKKEKLPKMRLLPTRSDMTCGYACLKGTAMKNTKRGSWYLEALQVFESE 379  
QY 216 KKGS--ILELTEITRLMANTFVMOEGKP---RYNPEVOSTLRKKLYL 259  
DB 380 RACDMHVAIDLKVNALLIKDREGYAPGTEFHRCKEMSEYCSLTCHNLYL 428

Search completed: February 26, 2003, 12:22:03  
Job time: 14.9841 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:16:30 ; Search time 27.9681 Seconds  
(without alignments)  
1915.475 Million cell updates/sec

Title: US-09-989-903-2  
Perfect score: 1350  
Sequence: 1 KPDMSEMSDPQLQGEERYD.....KPKKNPEVQSTLRKKLYIQ 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	295.5	21.9	423	13 Q91B67	Q91B67 xenopus lae
2	278	20.6	318	13 Q91B65	Q91B65 xenopus lae
3	278	20.6	403	13 Q90WU0	Q90WU0 gallus gall
4	276	20.4	220	11 Q90W14	Q90W14 mus musculu
5	274.5	20.3	435	4 Q9BUP7	Q9BUP7 homo sapien
6	274.5	20.3	452	11 Q95194	Q95194 ratcus norv
7	274	20.3	277	4 Q96A61	Q96A61 homo sapien
8	273	20.2	277	6 Q95ND5	Q95ND5 sus scrofa
9	272	20.1	277	4 Q96KP2	Q96KP2 homo sapien
10	266	19.7	282	13 Q98UI8	Q98UI8 brachydantio
11	265	19.6	454	11 Q98U70	Q98U70 mus musculu
12	264.5	19.6	303	11 Q88550	Q88550 ratcus norv
13	257	19.0	416	4 Q9B062	Q9B062 homo sapien
14	255	18.9	454	11 Q9JHK1	Q9JHK1 ratcus norv
15	254	18.8	399	13 Q91B63	Q91B63 xenopus lae
16	253	18.7	283	13 Q93417	Q93417 gallus gall

17	252	18.7	302	13 Q91B59	Q91B59 oncorhynch
18	246	18.2	182	6 Q77623	Q77623 ovis aries
19	245.5	18.2	476	13 Q91B33	Q91B33 brachydantio
20	242	17.9	480	11 Q89110	Q89110 m caspase 8
21	241	17.9	304	13 Q93415	Q93415 gallus gall
22	241	17.9	482	11 Q9JHX4	Q9JHX4 ratcus norv
23	240.5	17.8	293	4 Q9B0E7	Q9B0E7 homo sapien
24	240.5	17.8	520	13 Q91B62	Q91B62 xenopus lae
25	238	17.6	417	5 Q9YIU6	Q9YIU6 pristionchu
26	237	17.6	276	11 Q9D089	Q9D089 mus musculu
27	234.5	17.4	482	13 Q90WU1	Q90WU1 gallus gall
28	234	17.3	276	11 Q99M47	Q99M47 mus musculu
29	233.5	17.3	277	11 Q35397	Q35397 ratcus norv
30	232	17.2	383	13 Q91B17	Q91B17 brachydantio
31	229	17.0	283	13 Q42284	Q42284 gallus gall
32	227	16.8	500	13 Q91B64	Q91B64 xenopus lae
33	223	16.5	326	5 Q9GV88	Q9GV88 hydra atten
34	222	16.4	496	4 Q9COK4	Q9COK4 homo sapien
35	220	16.3	538	4 Q8TD15	Q8TD15 homo sapien
36	219	16.2	303	13 Q91B66	Q91B66 xenopus lae
37	215.5	16.0	308	5 Q9NHP9	Q9NHP9 drosophila
38	215.5	16.0	308	5 Q9VET9	Q9VET9 drosophila
39	213.5	15.8	479	4 Q8W708	Q8W708 homo sapien
40	209	15.5	393	11 Q9R0S9	Q9R0S9 mus musculu
41	206	15.3	402	11 Q91W32	Q91W32 ratcus norv
42	205.5	15.2	347	5 Q9GV89	Q9GV89 hydra atten
43	203	15.0	373	11 Q91XW7	Q91XW7 ratcus norv
44	200	14.8	420	11 Q920D5	Q920D5 ratcus norv
45	196	14.5	404	13 Q9DDJ2	Q9DDJ2 brachydantio

## ALIGNMENTS

### RESULT 1

ID	Q91B67	PRELIMINARY;	PRT;	423 AA.
AC	Q91B67;			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)			
DE	Caspase-2.			
GN	XCASPASE-2.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20209426; PubMed=10744739;			
RA	Nakajima K., Takahashi A., Yacita Y.;			
RT	"Structure, expression and function of the Xenopus laevis caspase			
RT	family.";			
RL	J. Biol. Chem. 275:10484-10491(2000).			
DR	EMBL; AB038168; BAA94746.1; -.			
DR	HSPR; P29466; 1ICE.			
DR	MEROPS; C14.006; -.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR002398; ICE.			
DR	InterPro; IPR002138; ICE_P10.			
DR	InterPro; IPR001309; ICE_P20.			
DR	Pfam; PF00619; CARD; 1.			
DR	Pfam; PF00655; ICE_P10; 1.			
DR	Pfam; PF00656; ICE_P20; 1.			
DR	PRINTS; PRO0376; IL1BCENZME.			
DR	SMART; SM00114; CARD; 1.			
DR	SMART; SM00115; CASc; 1.			
DR	PROSITE; PSS0209; CARD; 1.			
DR	PROSITE; PSS0122; CASPASE_CYS; 1.			
DR	PROSITE; PSS0121; CASPASE_HIS; 1.			
DR	PROSITE; PSS0207; CASPASE_P10; 1.			
DR	PROSITE; PSS0208; CASPASE_P20; 1.			

SQ SEQUENCE 423 AA; 47123 MW; E91EB1FD13F01FD CRC64;

Query Match 21.9%; Score 295.5; DB 13; Length 423;  
 Best Local Similarity 27.0%; Pred. No. 2,7e-16;  
 Matches 84; Conservative 58; Mismatches 104; Indels 65; Gaps 10;

QY 2 PDMESEMSDP-----OPLQERYDMSGARLALTLC-----VTKARE----- 37  
 DB 114 PVQESTLSRPGHQICREYREESIDDDGDPVTLQCSVNFYITHCOQAYKMHSCPRGRALL 173  
 QY 38 -----GSEVDMALERMFRYLKFESTMKDPPTAQOQLELDEFQOQITDWM 82  
 DB 174 ISNVKFEPTDLDYRCGGEVDLASLEKLFSLSLGYQVAVRCNLNAQSMQSLGAFSAL---- 229  
 QY 83 EEPVSCAF-----VLMAGHEEGLKGEDEKMYLEDFEVLNNKNCKALRGKPKVYIQA 138  
 DB 230 --PVHSALDSCVVALISHLDGAVYGTGKLVQLOQEVFALDINAHPQIQNKPKMFIOA 287  
 QY 139 CGEHRDPGEELRGNEELG-----DEELGDEVAVLKNNPOSIPYTDTLHIYSTVEGY 193  
 DB 288 CGEETDRGVDRDQREQSGSPCEQSDAGREDIKV-----RLPTQSDMICAVACTLKG 341  
 QY 194 LSYRDEKSGSGFIQTLTDVFI-HKKS-LLELTETRLMANTVWQEGKP---RVNPE 248  
 DB 342 VSLRNTKRSWFVQDLVSFQSHSKDTHVADMLKVNALIKEREGHAPETFRCKEMSE 401  
 QY 249 VOSTLRKKLYL 259  
 DB 402 YCSTLCRDLYL 412

RESULT 2

ID Q91B65 PRELIMINARY; PRT; 318 AA.

AC Q91B65:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Caspase-7.  
 GN XCASPASE-7.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 CC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20209426; PubMed=10744739;  
 RA Nakajima K., Takahashi A., Yaoita Y.,  
 RT "Structure, expression and function of the Xenopus laevis caspase  
 family";  
 RL J. Biol. Chem. 275:10484-10491(2000).  
 DR EMBL, AB038170; BAA9748.1; --.  
 DR HSSP, P42574; IPAU.  
 DR MEROPS, C14.004; --.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam, PF00655; ICE\_p10; 1.  
 DR Pfam, PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; ILIBENZYM.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 318 AA; 35937 MW; 6EBCE684AF86A128 CRC64;

Query Match 20.6%; Score 278; DB 13; Length 318;  
 Best Local Similarity 32.9%; Pred. No. 5,2e-15;  
 Matches 77; Conservative 39; Mismatches 96; Indels 22; Gaps 7;

QY 35 AREGEVDMALERMFRYLKFESTMKRDPPTAQOQLELDEFQOQITDWMEEPVSCAFV-VL 93

DB 97 ANGTIDIDARELLRCFKGEGFVNYYNNKSC---EEMENLRTVAQODHKDSACFACIF 152  
 QY 94 MHAGEGLKGEDEKMYLEDFEVLNNKNCKALRGKPKVYIQA CGEHRDPGEELGN 153  
 DB 153 LSHGEGGLYIGTGAM-PIKVLTTLPFGDNCRSLVGKRPFLFIQACRGHEPDDG----- 205  
 QY 154 EELGDEELGDEVAVLKNNPOSIPYTDTLHIYSTVEGYLSYRDEKSGSGFIQTLTDVF 213  
 DB 206 --LEADSGSVNDSLETDANPRHIKIVEADFLYASTVGYSMRPNQSMFVQALCSV- 262  
 QY 214 IHKKSILELTETR---LMANTVWQEGKP---RVNPEVOSTLRKKLYLQ 260  
 DB 263 INEYKELEVMQILTRVNFVATQPEYSDDPQFSKKQIPICVSMLTRKELYFK 316

RESULT 3

ID Q90WU0 PRELIMINARY; PRT; 403 AA.

AC Q90WU0:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Caspase 9 (Fragment).  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barton S., Bridgham J.T., Johnson A.L.;  
 RT "Caspase-8 and -9 expression in the hen ovary";  
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, AY057940; AAL23701.1; --.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR InterPro: IPR001993; Mitoch\_carrier.  
 DR Pfam, PF00619; CARD; 1.  
 DR Pfam, PF00655; ICE\_p10; 1.  
 DR Pfam, PF00656; ICE\_p20; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
 FT NON\_TER  
 SQ SEQUENCE 403 AA; 44913 MW; 0F1E40C3E6594FC4 CRC64;

Query Match 20.6%; Score 278; DB 13; Length 403;  
 Best Local Similarity 28.2%; Pred. No. 7e-15;  
 Matches 87; Conservative 44; Mismatches 106; Indels 72; Gaps 9;

QY 1 KPDMESMSDPOLQOERYDMSGARLALTLCV-----TKAREGSE 40  
 DB 112 QPESERFRMPAPAGSADVSKRPTDWCSCQTCCHLIFFNNVSFRRSDLSLRASD 171  
 QY 41 VDMALERMFRYLKFESTMKRDPPTAQOQLELDEFQOQITDWMEEPVSCAFVLMAGHEE 99  
 DB 172 ICEKLEKRFSLCFHVATLRLKAQEI DVELRLKLAR-LDH--SALDCCLVYLISHGCT 228  
 QY 100 -----GLKGEDEKMYLEDFEVLNNKNCKALRGKPKVYIQA CGEHRDPGEEL--- 150  
 DB 229 SHIOPGGIYGTGKITPIERLVNYFNQSQCSLGRKRLFFIOACGGEQKQGEVQCE 288  
 QY 151 -----RGNEELGDEELGDEVAVLKNNPOSIPYTDTLHIYST 189  
 DB 289 SPQDETCSRISDAIIPQAPSGNE---DEP---DAYA-----SLTPEDILVYST 334  
 QY 190 VEGYLSYRDEKSGSGFIQTLTDVFIHKKSILELTETRLMANTVWQEGKPKRVNPEV 249

DB	335	FRGFVSRMDKXVSGSVYVETLDSVLEHYARS	----	EDLTLTKLRVSDIVSSKRRYKQIPQC	390
Qy	250	QSTLRKLY 258			
Db	391	FNFLRKTF 399			
RESULT 4					
ID	Q9QW14	PRELIMINARY;	PRT;	220 AA.	
AC	Q9QW14;				
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)			
DE	CP32 apolpotic protease (fragment).				
GN	CASP3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RA	Denis F., Alm A., Cohen L., Hartgers F., Braun M., Martinez O.,				
RA	Fortin J.-P., Sekaly R.-P.,				
RT	"Multiple Pathways of Apoptosis Converging on the CPP32 Protease."				
RL	Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; U63720; AAD09504.1; -				
DR	HSSP; P42574; 1PAU.				
DR	MEROPS; C14.003; -				
DR	MCD; MG1.107739; Caep3.				
DR	InterPro; IPR002398; ICE.				
DR	InterPro; IPR002138; ICE_p10.				
DR	InterPro; IPR001309; ICE_p20.				
DR	Pfam; PF00655; ICE_p10; 1.				
DR	Pfam; PF00656; ICE_p20; 1.				
DR	PRINTS; PR00376; TLBCENZYM.				
DR	SMART; SM00115; CASC; 1.				
DR	PROSITE; PS01122; CASPASE_CYS; 1.				
DR	PROSITE; PS01121; CASPASE_HIS; 1.				
DR	PROSITE; PS50207; CASPASE_P10; 1.				
DR	PROSITE; PS50208; CASPASE_P20; 1.				
KM	Protease.				
FT	NON_TER				
SQ	SEQUENCE 220 AA; 25050 MW; FE7F4857CAEBA544 CRC64;				
Query March 20.4%; Score 276; DB 11; Length 220;					
Beet local similarity 33.3%; Pred. No. 4,8e-15;					
Matches 79; Conservative 39; Mismatches 81; Indels 38; Gaps 9					
Qy	35	AREGSEVMEALERFRFYKFEFSTMKRDPFAQFLDELDFQOTIDNMEEPSCAFV-VL 93			
Db	6	ARNGIDVDAANRERFMGLKTYQRKNDLTREDILEMD----SVSKESHKSRSSVVCYI 61			
Qy	94	MAHGEGLLKGEDEKVRLEDLFEVLNNKNCALRGKPRVYIIQACRGHRDPGEELRGN 153			
Db	62	LSHGEGVYGTNGP-VELKKLTSFPRGDYCSLTGKPKLFIIQACRGTELDGIE---- 116			
Qy	154	BEIGGDEBELGDEGVAVLKNPQSIPTTDTLHLYSVVEGLSYRDEKSGSFTQTLTD-- 211			
Db	117	TDSGDEDEAA-----CQKIPVADPLVAYSTAPGYVSWRNSKDSWFTQSICSMI 166			
Qy	212	-VFIRKKGSLLELTBEITFLMANTENVMOEGK-----PRKVNPEVOSTLRKLY 258			
Db	167	KLYARK----LQFMILTRV--NRKVATPEFSPSLDSTFHAKQKQFCIVSMLTKEYI 217			
RESULT 5					
ID	Q9BUP7	PRELIMINARY;	PRT;	435 AA.	
AC	Q9BUP7;				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			

	DE	Similar to caspase 2.
	OS	Homo sapiens (human).
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	OX	NCBI_TaxId=9606;
	RN	[1]
	RP	SEQUENCE FROM N.A.
	RC	TISSUE=SKIN;
	RA	Strauberg R.;
	RL	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
	DR	EMBL; BC002427; AAH02427.1; -
	DR	HSSP; P29466; IICE
	DR	IinterPro; IPRO01315; CARD.
	DR	IinterPro; IPRO02398; ICE.
	DR	IinterPro; IPRO02138; ICE_P10.
	DR	IinterPro; IPRO01309; ICE_P20.
	DR	Pfam; PF00619; CARD_1.
	DR	Pfam; PF00655; ICE_P10; 1.
	DR	Pfam; PF00656; ICE_P20; 1.
	DR	PRINTS; PRO0376; ILICENZYM.
	DR	SMART; SMO0114; CASC; 1.
	DR	SMART; SMO0115; CASC; 1.
	DR	PROSITE; PSS0209; CARD_1.
	DR	PROSITE; PS01122; CASPAGE_CYG; 1.
	DR	PROSITE; PS01121; CASPAGE_HIS; 1.
	DR	PROSITE; PSS0207; CASPAGE_P10; 1.
	DR	PROSITE; PSS0208; CASPAGE_P20; 1.
	SQ	SEQUENCE 435 AA; 48869 MW; 10CFA5AIP936E57 CRC64;
	Query Match:	20.3%; Score 274.5; DB 4; Length 435;
	Best Local Similarity	29.7% Pred. No. 1.5e-14;
	Matches 68; Conservative 51; Mismatches 103; Indels ?; Gaps 4;	
Dy	36 REGSVDMEEALERMFRYLKPESTMKRDPTAOOFELDEFODTIDNEEPVSCAFVLMA	95
Dd	:   :   :   :   :   :   :   :   :	
Dd	202 RSSGDVDNSTLVTLTKLGIVDHVLCDDTAOGMEKLONFMQ-LPAHYVTBSC-IVALLS	259
OY	96 HGEBSGLKGEDENKWRLEDLEFLVINNNKKCKALKRGPKYYIIQAACGRHRDPGEELRGNIE	155
Dd	:   :   :   :   :   :   :   :   :	
Dd	260 HGVEAGATIGVDGDKLLQLQDEVFQLPFNMANCPSLQNKPKNFFIOAQCGDGTDFGVQQDGGIN	319
OY	156 LGGDELLEGDEVAVALAKNNPOSTPIYTDTLTLYISTYEGLSTRHDKEGGSGFIOTLTDTVTH	215
Dd	:   :   :   :   :   :   :   :   :	
Dd	320 HAGSPGCESPDAAGEKLPKRMLPTSDMICGYACLKTGAAMRKNTKRSWYTEALLAQVFSE	379
OY	216 KKS--ILLETETIRLMANTENVNGEK---RKNPVGOSTLRKKYL	259
Dd	: : : : :   :   :   :   :   :   :   :   :	
Dd	380 RACMDHVADMLVKVALIKDRBGYAFTGFPHRCXMSEYSTLCRHLYL	428
	:	
	RESULT 6	
	CS5194 PRELIMITARY; PRT; 452 AA.	
ID	055194	
AC	055194;	
DT	01-JUN-1998 (TREMBLrel. 06, Created)	
DI	01-JUN-1998 (TREMBLrel. 06, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	NBD2/ICH-1.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
OX	NCBI_Taxid=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RE	MEDLINE=98087427; PubMed=9427555;	
RX	Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;	
RA	"Cloning and expression of the cDNA encoding rat caspase-2." ;	
RT	Gene 202:127-132(1997).	
RL	[2]	
RN	Sequence from N.A.	
RC	STRAIN=SPRAGUE-DAWLEY, TISSUE=BRAIN;	
RI	Jin K.L., Simon R.P., Graham S.H.;	
RU	Submitted (Mar-1999) to the EMBL/Genbank/DDBJ databases.	

DR EMBL; U77933; AAB96379.1; -.  
 DR EMBL; AF136231; AAD3684.1; -.  
 DR HSSP; P29466; IICE.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR002398; ICF.  
 DR InterPro; IPR002138; ICE\_p10.  
 DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; I1BCENZYM.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 452 AA; 50728 MW; 03F9D096BB741CE3 CRC64;

Query Match 20.3%; Score 274.5; DB 11; Length 452;  
 Best Local Similarity 30.6%; Pred. No. 1,6e-14;  
 Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

QY 36 REGSEVDMELERMFYKFESTMKRDPPTAQOFLBELDFEQOTIDNMBEPVSCAFVILMA 95  
 Db 219 RSGGDVHTTLVTLFPLGLGYNVHLVYDQTAQEWQEKLNFAQ-LPAHRYVTDSCLVALIS 276  
 QY 96 HGEELGLGDEKRMRLLEFLVNNKNCALRGKRYVITIOACGEHDPG---ELRG 152  
 Db 277 HGEELGIGVDKLLQLOLVFRLFDNANCPSLQNKPKMFIIACRDEDFRDVQDQDGN 336  
 QY 153 NEELGDEELGDEVAVLKNNPOSIPYTDTHIYSTEVEGLSYRHDEKSGFIQTLTDV 212  
 Db 337 HAQSGCGCESDQKXELMK---MRLETRSDMLCGYACLKGNAMNTRKSGSVIELTQV 393  
 QY 213 FIHKKS--ILELTEITRLMANTEVMOEGK--RKVNPEVOSTLRKKLYL 259  
 Db 394 FSERACDMHVALVKNVNLIKEREQYAPGTEFHRCKEWEVCSTLCQQLYL 445

## RESULT 7

Q96AN1 PRELIMINARY; PRT; 277 AA.  
 AC Q96AN1;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical 31.6 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LYMPH;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/genbank/DBJ databases.  
 DR EMBL; BC016926; AAH16926.1; -.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_p10.  
 DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; I1BCENZYM.  
 DR PROSITE; PS01122; CASPASE\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 277 AA; 31608 MW; 2F35CD3BC7FF64A CRC64;

Query Match 20.3%; Score 274; DB 4; Length 277;

Best Local Similarity 31.5%; Pred. No. 9.3e-15;  
 Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;  
 QY 6 SEMSDPQLQGERRYMSGARLALTLCVTK-----AREGSEVDMELERMFYKFP 55  
 Db 24 SEMSDSGISLDSNYMDPPEMGLCIINNNKFNKSTGTSSTSGTDVDANLRFTFRNLKY 83  
 QY 56 ESTMKRDPPTAQOFLBELDFEQOTIDNMBEPVSCAFV-VLMAHGEELGLGDEKRVRLD 114  
 Db 84 EVRNKNDLTR---BEIELMRDVSKEKDSKRSFVCLSHGEGILFTNGP-VDLKK 138  
 QY 115 LFEVLNNKNCALRGKRYVITIOACRGEHRDPGEELRGNEELGDEELGDEVAVLKNNP 174  
 Db 139 ITNFFRGDRCSRLTGKPKLFIIOACRGTLDGIE---TDSGV---DDMACHK--- 186  
 QY 175 QSIPTVTDTHIYSTEVEGLSYRHDEKSGFIQTLTDVFIHKKSILELTEITRLMANT 234  
 Db 187 --IPEADFLVAYSTAPGYVSRNKSQGSWFTQSLC-MLKQYADKLEFPHILITRV--NR 241  
 QY 235 EYMOEGK-----PRKNPEVOSTLRKKLY 258  
 Db 242 KVATFESESPDPTFAKKQIPCIYSMLTKELY 274

## RESULT 8

Q95ND5 PRELIMINARY; PRT; 277 AA.  
 AC Q95ND5;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Caspase-3.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxId=9623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21334413; PubMed=11440638;  
 RA Muneta Y., Shimotojima Y., Mori Y.;  
 RT "Porcine caspase-3: cloning and its activity during apoptosis of  
 RT porcine PK15 cells induced by porcine Fas-ligand."  
 RJ J. Interferon Cytokine Res. 21:409-415(2001).  
 DR EMBL; AB029345; BAB5544.1; -.  
 DR MEROPS; C14.003; -.  
 DR InterPro; IPR002138; ICE\_p10.  
 DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 20.2%; Score 273; DB 6; Length 277;  
 Best Local Similarity 31.8%; Pred. No. 1.1e-14;  
 Matches 83; Conservative 34; Mismatches 100; Indels 44; Gaps 9;

QY 19 YDMGARLALTLCVTK-----AREGSEVDMELERMFYKFESTMKRDPPTAQOF 68  
 Db 37 YMDYPEMGLCIINNNKFNKSTGTSSTSGTDVDANLRFTFRNLKYEVNRKNDLTR-- 93  
 QY 69 LEELDFEQOTIDNMBEPVSCAFV-VLMAHGEELGLGDEKRVRLDLEFLVNNKNCAL 127  
 Db 94 -BEIELMHSVSKEDSKRSFVCLSHGEGKFTNGP-VDLKLTLSFRRGCCRTL 151  
 QY 128 RCKPKYVITIOACRGEHRDPGEELRGNEELGDEELGDEVAVLKNNPOSIPYTDTHIY 187  
 Db 152 TCKPKLFIIOACRGTLDGIEITDSCGTE-----DDMC-----QKIPENAFVAY 197  
 QY 188 STEVEGLSYRHDEKSGFIQTLTDV--FIHKKSILELTEITRLMANTEVMOEG---- 240



Db 198 STAGYVSWRNSKDSWFIOSLCAALKOYHK---LEMLILTRVNRKVAPEFSFSTD 253  
Qy 241 ---KPRKVNPEVOSTLRKKLY 258  
Db 254 STPHAKKOIPCIIVSMILTREL 274

RESULT 9  
Q96KP2 PRELIMINARY; PRT; 277 AA.  
ID 096KP2  
AC 096KP2  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Caspase-3.  
GN CASP3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RA Vallette F.M.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Oliver L.J.;  
RT "Control of the activation of the procaspase-3 by a sequence located  
RT at the N-terminus of the p17 subunit."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ133269; CAC88866.1; -  
DR InterPro; IPR002398; ICE.  
DR InterPro; IPR002138; ICE\_p10.  
DR InterPro; IPR001309; ICE\_p20.  
DR Pfam; PF00655; ICE\_p10; 1.  
DR Pfam; PF00655; ICE\_p20; 1.  
DR PRINTS; PR00376; ILBENZYM.  
DR PROSITE; PS01122; CASPASE\_CYS; UNKNOWN\_1.  
DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
DR PROSITE; PS50207; CASPASE\_P10; 1.  
DR PROSITE; PS50208; CASPASE\_P20; 1.  
SQ SEQUENCE 277 AA; 31642 MW; 616276780DD2DE021 CRC64;

Query Match 20.1%; Score 272; DB 4; Length 277;  
Best Local Similarity 31.5%; Pred. No. 1,4e-14;  
Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

Qy 6 SEMSDPOLOEERYDMGALALTLCTK-----AREGSEVDMLEALERMFRYLF 55  
Db 24 SEMSDGMSWDTGYKMDYPEWGLCIINNNKNFHKSTGWTSGTDVDANLRETFRNLY 83  
Qy 56 ESTMKRDPDPAQFLEELDEFQOTIDNWEPRVCAFV-VLMHGEGLKGEDEKVRLED 114  
Db 84 EVRKAKNDITR---EELVELKRDVSKEDHSKRSSFVCLSHGEGGIIFTNGP-VDLKK 138  
Qy 115 LFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGDEELGDEVALKNP 174  
Db 139 ITNFFRGDRCSLTGCKPLFTIQCRCGTDLPGIE---TDSQVD---DDMACHK--- 186

Qy 175 QSIITYDTLHIYSTVEGYLSYRHDKSGFIQTLTDVFIHKKSILELTELRLMANT 234  
Db 187 --IIVDDAFLVAYSTAPYVSWRNSKDSWFIOSLC-AMLKQYADKLEFMHILTRV--NR 241

Qy 235 EVMQEGK-----PKAVNPEVOSTLRKKLY 258  
Db 242 KVATEFSFSFDATFHAKKOIPCIIVSMILTREL 274

RESULT 10  
Q98UI8 PRELIMINARY; PRT; 282 AA.  
ID 098UI8  
DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Caspase-3.  
GN CASP3.  
OS Brachydonto rexio (zebrafish) (zebra dario).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
[1]  
RP SEQUENCE FROM N.A.  
RA Yau T., Okazaki T., Yamashita M.;  
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to  
RT Mammalian Caspase-3."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB047003; BAB32409.1; -  
DR HSSP; P42574; 1PAU.  
DR MEROPS; C14.003; -  
DR ZFIN; ZDB-GENE-011210-1; casp3.  
DR InterPro; IPR002398; ICE.  
DR InterPro; IPR002138; ICE\_p10.  
DR InterPro; IPR001309; ICE\_p20.  
DR Pfam; PF00655; ICE\_p10; 1.  
DR Pfam; PF00655; ICE\_p20; 1.  
DR PRINTS; PR00376; ILBENZYM.  
DR SMART; SM00115; CASC; 1.  
DR PROSITE; PS01122; CASPASE\_CYS; 1.  
DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
DR PROSITE; PS50207; CASPASE\_P10; 1.  
DR PROSITE; PS50208; CASPASE\_P20; 1.  
SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;

Query Match 19.7%; Score 266; DB 13; Length 282;  
Best Local Similarity 29.2%; Pred. No. 4,4e-14;  
Matches 81; Conservative 46; Mismatches 104; Indels 46; Gaps 8;

Qy 9 SDPQLOEE-----RYDMSGARLALTLCTK-----KAREGSEVDMLEALERMFR 50  
Db 22 SASQPMQVDAKQSHARPRYSINYPNIGHCIINNNKFNDRRTGMNPRNGTDVDAGNMVNF 81  
Qy 51 RYLFESTMKRDPRPAQFLEELDEFQOTIDNWEPRVCAFV-VLMHGEGLKGEDEK 108  
Db 82 RKLGYIVKYNVDQFVAIMQVL-----TTVAHDHSCASLVCVLSHGEGVFEGTDT 136

Qy 109 MVRLEDLFEVLNNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEELGDEELGDEVA 168  
Db 137 -VDIKSLTSLFRGDRCSLVGCKPLFTIQCRCGTDLPGVETDHTD-----P 183

Qy 169 VLKNNPQSIPTTYDTLHIYSTVEGYLSYRHDKSGFIQTLTDVFIHKKSILELTEL 228  
Db 184 DIPDGRERIPVEADFLVAYSTAPYVSWRNSKDSWFIOSLCEN-MTKYSELELLQIMT 242

Qy 229 RL-----MANTVWQEGKPKVNPVOSTLRKKLY 258  
Db 243 RVNHKVALDEFSTSNMGPFAKKOIPCIIVSMILTREL 279

RESULT 11  
Q9ROT0 PRELIMINARY; PRT; 454 AA.  
ID 09ROT0  
AC 09ROT0  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Caspase3.  
GN CASP3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RP SEQUENCE FROM N.A.  
MEDLINE=20001956; PubMed=10529400;

RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikawa U., Momoi T.;  
 RT "Akt phosphorylation site found in human caspase-9 is absent in mouse  
 RT caspase-9";  
 RL Biochem. Biophys. Res. Commun. 264:550-555(1999).  
 DR EMBL; AB019600; BAAB695.1; -.  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.010; -.  
 DR MGD; MGI:1277950; Casp9.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002388; ICE\_p10.  
 DR InterPro; IPR01309; ICE\_p20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; ILBENZYM.E.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASc; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 DR SEQUENCE 454 AA; 50051 MW; 4614989AF823850F CRC64;  
 Query Match 19.7%; Score 266; DB 11; Length 454;  
 Best Local Similarity 31.0%; Pred. No. 8e-14; Indels 36; Gaps 9;  
 Matches 77; Conservative 46; Mismatches 89;  
 QY 36 REGSEVDMELERMFYLFKFESTMKRDPTAQOFLBELDFEQOTIDNMBEPVSCAFVILMA 95  
 Db 218 RTGSNLDRDKLEHFRMLRFVVEVKNDLTAKKVVATLMEMAH---RNHRALDCFVVILS 274  
 QY 96 HGEF-----GLKGDEKMWRLDELFEVLNNKCKALRGKPKVYIIQACRGHDPGE 148  
 Db 275 HCCQASHLQFPAYVYGTDCSVSIEKIVNI FNGSGCPSLGKPKLFFIQACGGEQDHGF 334  
 QY 149 ELRGNEBELGDELDGDEVAV-LKNNPQ-----SIPYTDLHIYSTVGYLSYRH 198  
 Db 335 EVACHTSSQCRITDSDSEPAVYQGEPRDLDDANVSLPTSDILVISTPGFVSMRD 394  
 QY 199 DEKSGGIQTLTDFVIHKKSILE--LTEITRLM--ANTENVQEGKPKRVNPEVOST 252  
 Db 395 KKSQGWYIEITL-----DGILEQWARSEDIQSLILRVANA-VSEKGYKKOI-PCGCFNF 444  
 QY 253 LRKXLYLQ 260  
 Db 445 LRKXLFK 452  
 RESULT 12  
 O88550 PRELIMINARY; PRT; 303 AA.  
 AC O88550;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Caspase-7.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RC Forghani F., Roy S.;  
 RT "Rat caspase-7 sequence";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF07124; AAC24011.1; -.  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.004; -.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002318; ICE\_p10.

DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; ILBENZYM.E.  
 DR SMART; SM00115; CASc; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 DR SEQUENCE 303 AA; 34324 MW; A71728754BF199DD CRC64;  
 Query Match 19.6%; Score 264.5; DB 11; Length 303;  
 Best Local Similarity 34.2%; Pred. No. 6.4e-14; Indels 25; Gaps 8;  
 Matches 79; Conservative 35; Mismatches 92;  
 QY 36 REGSEVDMELERMFYLFKFESTMKRDPTAQOFLBELDFEQOTIDNMBEPVSCAFVILMA 95  
 Db 87 RNGTHDKAEALFKCFRSLGFEVITYINDSCAKM---ODLRRASEEDHSNACFVILS 143  
 QY 96 HGEGLKGEDEKMWRLDELFEVLNNKCKALRGKPKVYIIQACRGHDPGEELRGNEE 155  
 Db 144 HGEENLIYKGD-GVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDG----- 194  
 QY 156 LGGEELGDEVAVLKNNPQ-SIPYTDLHIYSTVGYLSYRDEKSGGIQTLTDFVI 214  
 Db 195 IQADSGPIINDTDA---NPRYKIVEADFLFAYSTVGYYSWRNPGKSWFVALCSI-L 249  
 QY 215 HKKGSILELTELITRL--MANTENVQEGKPR---KVNPEVOSTLRKLY 258  
 Db 250 NEHGKLEIMQILTRVNDVARHFSQSDPRENEKKOIPCMVSLTKELY 300  
 RESULT 13  
 O9B062 PRELIMINARY; PRT; 416 AA.  
 AC O9B062;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Unknown protein for MOC:2105 (Caspase 9, apoptosis-related cysteine protease)  
 DE (MOC61).  
 DE CASP9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIMPH;  
 RC Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EYE;  
 RC Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Thomas D.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006463; AAH06463.1; -.  
 DR EMBL; BC002452; AAH02452.1; -.  
 DR EMBL; AL512883; CAC42423.1; -.  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.010; -.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002318; ICE\_p10.  
 DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.

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DR PRINTS, PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROTEASE.
SQ SEQUENCE 416 AA; 46280 MW; 78E0180DF2A3BDD2 CRC64;

Query Match 19.0%; Score 257; DB 4; Length 416;
Best Local Similarity 29.5%; Pred. No. 4e-13;
Matches 75; Conservative 46; Mismatches 89; Indels 44; Gaps 8;

QY 34 KAREGEVDMALERMRYLKFEESTMKRDPAAQFLBELDEFOQTINWEEPVSCAFVYL 93
DB 178 RRTGSIHIDCKLRKRRSSLHFMVYKGDLTAKKVLALLELAQDHG--ALDCCVAVI 234
QY 94 MARGEE-----GLKGEDEKVRLEDFEVLNNKCKALRGPKVYIIQACRGERHP 146
DB 235 LSHGCGASHLQFPGAVYGTGCPVSEKIVNI FNGTSCPSLGCKPKLPFIQACGEGQKH 294
QY 147 GBEIRKNEBELGDEBELGDEVAVLKNNPQ-----SIPTTDTLHI 186
DB 295 GFPEVASTSP--EDESFG-----SNPEPDATPFQGLRTFDQLDAISSLPSPDIFVS 344
QY 187 YSTVEGYLSYRHDKSGSGFIQTLTDVFIHKKSILELTETIRLMANTVMOEGKPRKVN 246
DB 345 YSTFPGVSNRDPKSGSWYETLDDIF--EQMAHSEDLQSLLRVANA-VSVKGIYKQM- 400
QY 247 PEVOSTLRKKLYLQ 260
DB 401 PGCFNPLRKKLFPK 414

RESULT 14
Q9JHK1 PRELIMINARY; PRT; 454 AA.
ID Q9JHK1;
AC Q9JHK1;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-9 (Caspase-9 long isoform).
GN RNCASP9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Cao G., Chen D., Pei W., O'Horo C., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Itoh T., Itoh A., Pleasure D.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=CEREBELLUM;
RA Cao G., Chen D., Graham S., Simon R.P., Chen J.;
RT "Cloning and Characterization of Rat Caspase-9: Implication for a Role
RT in Neuronal Cell Death During Brain Development and Transient Cerebral
RT Ischemia."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=21192275; PubMed=11278518;

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RA Angelastro J.M., Moon N.Y., Liu D.X., Yang A.-S., Greene L.A.,
RA Franke T.F.;
RT "Characterization of a Novel Caspase-9 Isoform in Rat That Inhibits
RT Apoptosis."
RL J. Biol. Chem. 276:12190-12200(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=MKY;
RX MEDLINE=21552893; PubMed=11695991;
RA Nishiyama J., Yi X., Venkatachalam M.A., Dong Z.;
RT "cDNA cloning and promoter analysis of rat caspase-9."
RL Biochem. J. 360:49-56(2001).
DR EMBL; AF262319; AAF85658.1; -
DR EMBL; AF271996; AAF76217.1; -
DR EMBL; AF286006; AAF99705.1; -
DR EMBL; AF304669; AAK31519.1; -
DR EMBL; AY027667; AAK26235.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50399 MW; 501623B29B6ED6FC CRC64;

Query Match 18.9%; Score 255; DB 11; Length 454;
Best Local Similarity 30.5%; Pred. No. 6.5e-13;
Matches 74; Conservative 49; Mismatches 94; Indels 26; Gaps 8;

QY 36 REGSEVDMALERMFRYLKEESTMKRDPYQQLBELDEFOQTITDWEVSCAFVYLMA 95
DB 218 RISHVDCEKLRHFCFLRMVAVKNDLTAKKVTALMENAH--RDHRLDCEVVILS 274
QY 96 HGEE-----GLKGEDEKVRLEDFEVLNNKCKALRGPKVYIIQACRGERHPGE 148
DB 275 HGCGASHLQFPGAVYGTGCGSVISIERIVNFNGTSCPSLGCKPKLPFIQACGEGQKHG 334
QY 149 EL--RGNEBELGDEBELGDEVAVLKNNPQ-----SIPTTDTLHIYSTVEGYLSYR 197
DB 335 EVAFTSQDKAFSDSEPDVPP-YQSGPRTLDDQDANVSSLPITSDILVYSTPFGFVSWR 393
QY 198 HDEKSGCFIOTLTDVFIHKKSILELTETIRLMANTVMOEGKPRKVNPEVOSTLRKKL 257
DB 394 DKXSGSWYETLDDGVL--EQMARSEDLQSLLRVANA-VSEKGIYKXI-PGCFNPLRKKL 449
QY 258 YLQ 260
DB 450 FPK 452

RESULT 15
Q9IB63 PRELIMINARY; PRT; 399 AA.
ID Q9IB63;
AC Q9IB63;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

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OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE=20209426; PubMed=10744739;  
 RA Nakajima K., Takahashi A., Yaita Y.,  
 RT "Structure, expression and function of the Xenopus laevis caspase  
 RT family";  
 RL J. Biol. Chem. 275:10484-10491(2000).  
 DR EMBL; AB038172; BAA94750.1; -.  
 DR HSSP; Q15806; IQDU.  
 DR MEROPS; C14.010; -.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_p10.  
 DR InterPro; IPR01309; ICE\_p20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; ILICENZVME.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;  
 SQ

Query Match 18.8% Score 254; DB 13; Length 399;  
 Best Local Similarity 28.0%; Pred. No. 6.6e-13;

Matches 78; Conservative 42; Mismatches 113; Indels 46; Gaps 9;

QY 15 QEERYDMSGARLALTLCVT-----KAREGSEVDMLEALRMFRYLKPESTMKRDPT 64  
 Db 132 KDKDYPMSDDPIGFLIIINNMNFHECTGLSTRTGSDIDRDKLANMRSPHFVTVKDNLT 191  
 QY 65 AQQFLLELDEFQQTIDNMEEPVSCAFVILMANGEE-----GLKGEDEKMRLEDLFE 117  
 Db 192 GQAM--HDHLQALADODHSLDCCLVILSHGCETRHIQFPGVYGTGDIRIPVERIVS 248  
 QY 118 VLNNKCKALRGKPKVYIIQACRGEHRDPGEELRG-----NEELGSD-----ELG 163  
 Db 249 YFNGSKCPSLRGKPKFIILQACGGDKDKGCEVTSETPLSTSTSLQSDATPVFSGED 308  
 QY 164 GDEVAVLKNNPOSIPYTDTLAIYSTVEGYLSYRHDEKSGFIQTLLTDVFIHKGSILEL 223  
 Db 309 RDEVDAVSN---IPTPSDILVSYSTFPGYVSWRDKHTGSMWYVEVLDVLAHHAA---- 360  
 QY 224 TBEITRL--MANTVMOEGKPRKANPEVOSTLRKLYLO 260  
 Db 361 -DDLQSLVWVADGVSSKGTYSKQI-PGYNPLRKRPYFK 397

Search completed: February 26, 2003, 12:20:28  
 Job time : 29.9681 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:14:00 ; Search time 8.19522 Seconds

(without alignments)  
1224.772 Million cell updates/sec

Title: US-09-989-903-5

Sequence: 1 MSNPRSLBEERKYMGSALAL.....KARKNPETQSTLRKRLYLQ 242

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1234	99.6	242	1	ICEE_HUMAN
2	934.5	75.4	257	1	ICEE_MOUSE
3	305	24.6	424	1	ICED_CHICK
4	295	23.8	435	1	ICED_MOUSE
5	289	23.3	435	1	ICED_HUMAN
6	279.5	22.6	277	1	ICED_RAT
7	277.5	22.4	277	1	ICED_CRITO
8	273.5	22.1	277	1	ICED_MOUSE
9	272.5	22.0	277	1	ICED_HUMAN
10	270	21.8	303	1	ICED_MOUSE
11	260	21.0	303	1	ICED_MOUSE
12	256	20.7	303	1	ICED_MOUSE
13	248.5	20.1	503	1	ICED_MOUSE
14	247.5	20.0	339	1	ICED_MOUSE
15	246.5	19.9	479	1	ICED_MOUSE
16	245	19.8	496	1	ICED_MOUSE
17	240.5	19.4	276	1	ICED_MOUSE
18	237.5	19.2	299	1	ICED_MOUSE
19	236.5	19.1	404	1	ICED_MOUSE
20	232.5	18.8	416	1	ICED_MOUSE
21	227	18.3	282	1	ICED_MOUSE
22	226.5	18.3	382	1	ICED_MOUSE
23	225.5	18.2	404	1	ICED_MOUSE
24	225.5	18.2	323	1	ICED_MOUSE
25	225	18.2	418	1	ICED_MOUSE
26	222.5	18.0	521	1	ICED_MOUSE
27	221.5	17.9	521	1	ICED_MOUSE
28	218.5	17.6	402	1	ICED_MOUSE
29	218	17.6	373	1	ICED_MOUSE
30	217.5	17.6	402	1	ICED_MOUSE
31	214	17.3	293	1	ICED_MOUSE
32	213.5	17.2	312	1	ICED_MOUSE
33	212.5	17.2	405	1	ICED_MOUSE

34	211	17.0	410	1	ICED_MOUSE
35	209	16.9	404	1	ICED_MOUSE
36	205.5	16.6	377	1	ICED_MOUSE
37	196	15.8	377	1	ICED_MOUSE
38	193.5	15.6	419	1	ICED_MOUSE
39	104.5	8.4	484	1	ICED_MOUSE
40	95.5	7.7	2104	1	ICED_MOUSE
41	94	7.6	480	1	ICED_MOUSE
42	91	7.3	510	1	ICED_MOUSE
43	91	7.3	510	1	ICED_MOUSE
44	90.5	7.3	520	1	ICED_MOUSE
45	89.5	7.2	1225	1	ICED_MOUSE

## ALIGNMENTS

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RESULT 1
ICED_HUMAN
ID ICED_HUMAN STANDARD; PRT; 242 AA.
AC P31944; O95823;
DT 01-JUN-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Pover J.-L., Srinivasula S.M., Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of human caspase 14."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Raamsen H.H., van Damme J., Puype W., Geeser B., Celis J.E.,
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RL protein database of normal human epidermal keratinocytes."
CC Electrophoresis 13:960-969 (1992).
CC -!- FUNCTION: MAY BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME B
APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL TRANSDUCER
OR CELL DEATH.
CC -!- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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DR EMBL: AF097874; AAD16173.1;
DR HSPR: P29466; ICED.
DR Aarhus/Chent-2PAGE; 6109; IEF.
DR MEROPS; C14.018;
DR Genew; HGNC:1502; CASP14.
DR MIM; 605848;
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_D20.
DR Pfam; PF00655; ICE_P10.1.
DR Pfam; PF00656; ICE_P20.1.
DR PRINTS; PR00376; ILCENZYME.
DR SMART; SM00115; CASP; 1.

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DR PROSITE; PS01121; CASPASE\_HIS; FALSE\_NEG.  
 DR PROSITE; PS01022; CASPASE\_CYS; FALSE\_NEG.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.  
 FT PROPEP 1 146 CASPASE-14 SUBUNIT 1 (POTENTIAL).  
 FT CHAIN ? 242 CASPASE-14 SUBUNIT 2 (POTENTIAL).  
 FT ACT SITE 89 89 BY SIMILARITY.  
 FT ACT SITE 132 132 BY SIMILARITY.  
 SQ SEQUENCE 242 AA; 27679 MW; E539FB7EBD908A2 CRC64;

Query Match 99.6%; Score 1234; DB 1; Length 242;  
 Best Local Similarity 99.6%; Pred. No. 7,8e-93;  
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 60  
 DB 1 MSNPRLSEEEKYDMSGALALILCTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 60  
 QY 61 FOEELKFOQADISREDPVSCAFVILMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120  
 DB 61 FOEELKFOQADISREDPVSCAFVILMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120  
 QY 121 RAKPRVYIIQACRGQRDPGEIVGVDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 180  
 DB 121 RAKPRVYIIQACRGQRDPGEIVGVDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 180  
 QY 181 DOKGSCFIOTLVDFVTFKRGHILELLETRMAENLVOEGKARKTNEIOSTLRKLY 240  
 DB 181 DOKGSCFIOTLVDFVTFKRGHILELLETRMAENLVOEGKARKTNEIOSTLRKLY 240  
 QY 241 LQ 242  
 DB 241 LQ 242

RESULT 2  
 ICEE\_MOUSE STANDARD; PRT; 257 AA.  
 AC 089054;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mm1-ICE) (MICE).  
 GN CASP14.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN 11  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=C57BL/6J; PubMed=9823333;  
 RX MEDLINE=99040667; PubMed=10203698;  
 RA Ahmed M., Srinivasula S.M., Hegde R., Mukattash R.,  
 RA Fernandes-Alnemri T., Alnemri E.S.;  
 RT "Identification and characterization of murine caspase-14, a new  
 RT member of the caspase family";  
 RL Cancer Res. 58:5201-5205(1998).  
 RN 12  
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Embryo;  
 RX MEDLINE=99222069; PubMed=10203698;  
 RA Van den Craen M., Van Loo G., Pye S., Van Crielinge W.,  
 RA Vandenbeele P.;  
 RT "Identification of a new caspase homologue: caspase-14";  
 RL Cell Death Differ. 5:838-846(1998).  
 RN 13  
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.  
 RX MEDLINE=99009076; PubMed=9792675;  
 RA Hu S., Snijpae S.J., Vincenz C., Salvesen G., Dixit V.M.;  
 RT "Caspase-14 is a novel developmentally regulated protease";

RL J. Biol. Chem. 273:29648-29653(1998).  
 CC -1- FUNCTION: SEEMS TO BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME  
 CC B APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL  
 CC TRANSDUCER OF CELL DEATH. MAY PLAY A ROLE IN ONTOGENESIS AND SKIN  
 CC PHYSIOLOGY.  
 CC -1- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- TISSUE SPECIFICITY: EMBRYO, ADULT LIVER AND LESS IN ADULT BRAIN  
 CC AND KIDNEY.  
 CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE  
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
 CC PROTEASE.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

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 CC -----  
 CC EMBL; AF092997; AAC83364.1; -;  
 CC EMBL; AJ007750; CAA07678.1; -;  
 CC HSSP; P29466; 1ICE.  
 CC MEROPS; C14.018; -;  
 CC MGD; MGI:1335092; Casp14.  
 CC InterPro; IPR002398; ICE.  
 CC InterPro; IPR002138; ICE\_P10.  
 CC InterPro; IPR001309; ICE\_P20.  
 CC Pfam; PF00655; ICE\_P10; 1.  
 CC Pfam; PF00656; ICE\_P20; 1.  
 CC SMART; SMO0115; CASC; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; FALSE\_NEG.  
 DR PROSITE; PS01122; CASPASE\_CYS; FALSE\_NEG.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.  
 FT PROPEP 1 7  
 FT CHAIN ? 257 CASPASE-14 SUBUNIT P18 (POTENTIAL).  
 FT ACT SITE 93 93 CASPASE-14 SUBUNIT P11 (POTENTIAL).  
 FT ACT SITE 136 136 BY SIMILARITY.  
 FT MUTAGEN 136 136 C->A: DECREASE IN DEATH-INDUCING  
 FT ACTIVITY.  
 SQ SEQUENCE 257 AA; 29458 MW; A228D88DDBA0EB84 CRC64;

Query Match 75.4%; Score 934.5; DB 1; Length 257;  
 Best Local Similarity 70.9%; Pred. No. 1.3e-68;  
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 60  
 DB 5 MSNPRLSEEEKYDMSGALALILCTKAREGSEEDLDALHMFRLRFRSTTKRPTAQ 64  
 QY 61 FOEELKFOQADISREDPVSCAFVILMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120  
 DB 61 FOEELKFOQADISREDPVSCAFVILMAHGREGLKGEDEGVKLENLFEALNNKCOAL 124  
 QY 121 RAKPRVYIIQACRGQRDPGEIVGVDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 180  
 DB 121 RAKPRVYIIQACRGQRDPGEIVGVDEIYMWIKDSPQIIPYTDALHYSTVEGYIAYRH 183  
 QY 181 DOKGSCFIOTLVDFVTFKRGHILELLETRMAENLVOEGKARKTNEIOSTLRKLY 228  
 DB 181 DOKGSCFIOTLVDFVTFKRGHILELLETRMAENLVOEGKARKTNEIOSTLRKLY 243  
 QY 229 PEIOSTLRKLYLQ 242  
 DB 244 PEVOSTLRKLYLQ 257

RESULT 3  
ID ICE2\_CHICK STANDARD; PRT; 424 AA.  
AC 098943;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-11/15).  
GN CASP2 OR ICH1.  
OS Gallus gallus (chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_Taxid=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White Leghorn; TISSUE=Ovarian granulosa;  
RX MEDLINE=97368127; PubMed=9224894;  
RA Johnson A.L., Bridgham J.T., Bergeron L., Yuan J.;  
RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary";  
RL Gene 192:227-233(1997).  
CC -|- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER  
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING  
CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).  
CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ICH-1L (SHOWN HERE) AND ICH-1S;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-  
CC TERMINI. ONLY THE ICH-1L FORM IS FOUND IN THE OVARY.  
CC -|- PTM: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
CC -|- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -----  
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CC -----  
DR EMBL; U64963; AAC29881.1; ALT\_INIT.  
DR HSSP; P42574; ICP3.  
DR MEROPS; C14.006; -.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR002398; ICE.  
DR InterPro; IPR002138; ICE\_P10.  
DR InterPro; IPR001309; ICE\_P20.  
DR Pfam; PF00619; CARD.1.  
DR Pfam; PF00655; ICE\_P10.1.  
DR Pfam; PF00656; ICE\_P20.1.  
DR PRINTS; PR00376; TLBCENZTME.  
DR SMART; SM00114; CARD.1.  
DR SMART; SM00115; CARD.1.  
DR PROSITE; PS50209; CARD.1.  
DR PROSITE; PS01122; CASPASE\_CYS.1.  
DR PROSITE; PS01121; CASPASE\_HIS.1.  
DR PROSITE; PS50207; CASPASE\_P10.1.  
DR PROSITE; PS50208; CASPASE\_P20.1.  
KM Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.  
FT PROPEP 1 140  
FT CHAIN 141 308 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).  
FT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).  
FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).  
FT DOMAIN 7 96 CARD.  
FT ACT\_SITE 248 248 BY SIMILARITY.  
FT ACT\_SITE 291 291 BY SIMILARITY.  
FT VARSPIC 1 7 MISSING (IN ISOFORM ICH-1S).  
FT VARSPIC 294 424 DETROGDQDRGKRSRSDSGEESDANKENLKLRLPFRSD  
MITGACLKGTAAKRNTRGWSYIEALTYFAEDSRTHVA  
DMLVKVRQIKRGVAGTEFHRCKEMSEYCTLCRDLYL  
PPGVPGK -> GVSIGIHILPLCCCHICCSMRQGEWI

FT REMARK:GQIPQAVRRVWQTRKTKISSCVCLHAPI (IN  
FT ISOFORM ICH-1S).  
SQ SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;  
Query Match 24.6%; Score 305; DB 1; Length 424;  
Best Local Similarity 31.5%; Pred. No. 1.9e-17;  
Matches 86; Conservative 51; Mismatches 82; Indels 54; Gaps 10;  
QY 1 MSNPRSLSEEEKYDMSGALALILC-----VTKAREGSEEDIDALEHMPROLPFESTM 52  
DB 166 ISEPR-----GLAILLSNIHFSSSEKDELYSGGDVDCASLEFLFKHLYGYTV 213  
QY 53 KRDPFAQFOEELKFOQALIDSRDPVSCAFVLMAGREGFLKGDGEWYKLENLEAL 112  
DB 214 PHDQSAEEMSGALERFSKLPD-HQDVDS-C-IVALLSHGVGEGVYGTQKLLQLQEAFFLF 271  
QY 113 NKKGCQALRAKPKYITIOACRGEDRPG-ETVGDDELVMYIKDSP-----Q 157  
DB 272 DNANCPMLQNKPKMFFIOACGDETDGVDQDSKE---RSDSPGCEESDANKENLKL 327  
QY 158 TIPTYALHVSVEGVIAVRHDQKSCFIOTLVDFTK--RKHILLETVEYRMAE 215  
DB 328 RLPTRSDMICYACKLTGAAMRNTRKRSWYIEALTYFAEDSRTHVADMLVKVRQIKQ 387  
QY 216 AELVQEGKARKTN-----PEIQSTLRKRLYL 241  
DB 388 ---REGVAPGTEFHRCKEMSEYCTLCRDLYL 416  
RESULT 4  
ID ICE2\_MOUSE STANDARD; PRT; 435 AA.  
AC P29594; O08737;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 DE protein).  
GN CASP2 OR ICH1 OR NEDD2 OR NEDD2-2.  
OS Mus musculus (mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c.  
RX MEDLINE=95047319; PubMed=7958843;  
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;  
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a  
RT protein similar to the product of the Caenorhabditis elegans cell  
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";  
RL Genes Dev. 8:1613-1626(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/An;  
RX MEDLINE=97190206; PubMed=9038361;  
RA van de Graen M., Vandenabeele P., Declercq W., van den Brande I.,  
RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,  
RA Fiers W.;  
RT "Characterization of seven murine caspase family members";  
RL FEBS Lett. 403:61-69(1997).  
RN [3]  
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92328780; PubMed=1378265;  
RA Kumar S., Tomooka Y., Noda M.;  
RT "Identification of a set of genes with developmentally down-regulated  
RT expression in the mouse brain.";  
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).  
CC -|- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER  
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING  
CC PROTEINS NECESSARY FOR CELL SURVIVAL. MAY BE IMPORTANT IN

```

CC MULTISTEP CARCINOGENESIS.
CC SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGH LEVEL EXPRESSION SEEN IN THE EMBRYONIC
CC CNS, LIVER, LUNG, KIDNEY, SMALL INTESTINE, AND HAIR FOLLICLES OF
CC VIBRISSEAE. MODERATE EXPRESSION SEEN IN THE SKIN, ORAL MUCOSA,
CC SKELETAL MUSCLE, SUBMANDIBULAR GLAND AND THYMUS. IN THE ADULT, IT
CC IS HIGHLY EXPRESSED IN SPLEEN, LUNG AND KIDNEY. MODERATELY IN THE
CC BRAIN, HEART, TESTIS, LIVER. LOW LEVELS IN THE THYMUS, SKELETAL
CC MUSCLE, OVARY AND GUT.
CC -1- DEVELOPMENTAL STAGE: DURING EMBRYONIC DEVELOPMENT IS HIGHLY
CC EXPRESSED IN SEVERAL TYPES OF MOUSE TISSUE UNDERGOING HIGH RATES
CC OF PROGRAMMED CELL DEATH SUCH AS CENTRAL NERVOUS SYSTEM AND
CC KIDNEY.
CC -1- PM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -----
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CC -----
CC EMBL; D28492; BA25876.1; ALT_INIT.
CC EMBL; Y13085; CA473527.1; ALT_INIT.
CC HSSP; P42574; ICP3.
CC MEROPS; C14.006; -.
CC MGD; MGI:97295; Casp2.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_p10.
CC InterPro; IPR001309; ICE_p20.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00655; ICE_p10; 1.
CC Pfam; PF00656; ICE_p20; 1.
CC PRINTS; PR00376; IILBENZYM.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00115; CASC; 1.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS0207; CASPASE_P10; 1.
CC PROSITE; PS0208; CASPASE_P20; 1.
CC K1M HydroLase; Thiol protease; Apoptosis; Zymogen.
CC PROPEP 1 152
CC CHAIN 153 316
CC CHAIN 317 435
CC CHAIN 331 435
CC DOMAIN 15 103
CC ACT_SITE 260 260
CC ACT_SITE 303 303
CC MUTAGEN 303 303
CC CONFLICT 71 71
CC SEQUENCE 435 AA; 48896 MW; 8984E6AA76E7676 CRC64;

Query Match 23.8%; Score 295; DB 1; Length 435;
Best Local Similarity 31.5%; Pred. No. 1.2e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

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Db 320 HTSPGCEESDAGKEELMKR-----LPTSRDMICGVACLKGNAAMRNTKSGMYIEALT 374
Cy 193 DVETKR--KGHLELLTEVTRMAEALVQEGKAKTN-----PEIOSTLRKRLYL 241
Db 375 QVFSERACDMHVDMLVYNALIKE---RGYAPGTEFHCKEMSEYSCITLCOOLYL 428

RESULT 5
ID ICE2_HUMAN STANDARD; PRT; 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
DE 1L/1S).
GN CASP2 OR ICH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=94373811; PubMed=8087842;
RT Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;
RT "ich-1, an ice/ced-3-related gene, encodes both positive and negative
RT regulators of programmed cell death.";
RL Cell 78:739-750(1994).
RN [2]
RP CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shahan S., Horvitz H.R.;
RT "The Caenorhabditis elegans cell death protein CED-3 is a cysteine
RT protease with substrate specificities similar to those of the human
RT Cpp32 protease.";
RL Genes Dev. 10:1073-1083(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER
CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING
CC PROTEINS NECESSARY FOR CELL SURVIVAL.
CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ICH-1L (SHOWN HERE) AND ICH-1S;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-
CC TERMINI. ICH-1L ACTS AS A POSITIVE REGULATOR OF APOPTOSIS, WHEREAS
CC ICH-1S FUNCTIONS AS A NEGATIVE REGULATOR OF APOPTOSIS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LARGER AMOUNTS IN THE EMBRYONIC
CC LUNG, LIVER AND KIDNEY THAN IN THE HEART AND BRAIN. IN THE ADULTS
CC HIGHER LEVEL EXPRESSION IS SEEN IN THE PLACENTA, LUNG, KIDNEY,
CC PANCREAS THAN IN THE HEART, BRAIN, LIVER AND SKELETAL MUSCLE.
CC -1- PM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U13021; AA58959.1; -.
CC EMBL; U13022; AA58960.1; -.
CC HSSP; P29466; IICE.
CC MEROPS; C14.006; -.
CC Genew; HGNC:1503; CASP2.
CC MIM; 600639; -.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002398; ICE.
CC InterPro; IPR002138; ICE_p10.

```



DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR PRINTS: PR00376; IL1BCENZME.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00115; CASC; 1.  
 DR PROSITE: PS50209; CARD; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.  
 FT PROPEP 1 152  
 FT CHAIN 153 308 CASPASE-2 SUBUNIT P18.  
 FT PROPEP 309 316  
 FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.  
 FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.  
 FT DOMAIN 15 103 CARD.  
 FT ACT\_SITE 260 260 BY SIMILARITY.  
 FT ACT\_SITE 303 303 BY SIMILARITY.  
 FT VARSPIC 1 14 MISSING (IN ISOFORM ICH-1S).  
 FT VARSPIC 306 435 DETROGVDQDQGNKHAASPGCESDAKKLPKRLPTRSD  
 MTCGACLCGTAARNTKRGSWYLEALQVFSEKCMHVA  
 DMLVKNVALIKDRGVAPGTEFHRCKEMSEYCSLCHRLYL  
 FPGHPT -> GGAIGSLGHLLEFTATASIAL (IN  
 ISOFORM ICH-1S).  
 FT MUTAGEN 303 303 C-S: LOSS OF FUNCTION.  
 FT MUTAGEN 352 352 A-T: LOSS OF FUNCTION.  
 SQ SEQUENCE 435 AA; 4885 MW; 1652EC7JF6286F87 CRC64;  
 Query Match 23.3%; Score 289; DB 1; Length 435;  
 Best Local Similarity 31.1%; Pred. No. 3.8e-16;  
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;  
 QY 29 REGSEEDIDALEHMPROIFESTMKRDTAFOFDELEKFOQADISREDPVSCAFVILMA 88  
 DB 202 RSGGDVHSTLVTLFKLGDVHVHLCDDTAQDMQEKLNFAQ-LPAHVTDSCLVALLS 259  
 QY 89 HGRSGFLKGESEVAVKLELFEALNNKCOALBAKPKYIIIOARGGDRDG----- 140  
 DB 260 HGVEGALIVGDKLQLOEVLPDNANCPSLQNPKNPFQDQCGDGTDRGVDOQDGN 319  
 QY 141 -----ETVGDDEIVWIKDSPTIPTYDALHVSVEGYIAYRHDOGSCFIOTLV 192  
 DB 320 HAGSPGCESSAGKE-----KLPRKRLPTRSDMTCGACLCGTAARNTKRGSWYLELA 374  
 QY 193 DVFTKR-KGHLLELTVTRMADELIVGCKARKTN-----PEIQSLTKRKLVL 241  
 DB 375 QVFSEKADCMHVAQDMLVKNVALIKD---REGVAPGTEFHRCKEMSEYCSLCHRLYL 428  
 RESULT 6  
 ICES\_RAT STANDARD; PRT; 277 AA.  
 ID ICES3\_RAT P55213; Q62993; P97699;  
 AC P55213; P70543; Q62993; P97699;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama  
 protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)  
 DE (SCA-1) (LICE) (IRP).  
 GN CASP3 OR CPP32.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eultheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96358624; PubMed=8761296;  
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
 RA Fletcher F.A.;  
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding

RT a cysteine protease resembling interleukin-1 beta converting enzyme  
 RT and CED-3.";  
 RL Oncogene 13:749-755 (1996).  
 RN [2]  
 RN SEQUENCE OF 30-241 FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=96042508; PubMed=7588240;  
 RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,  
 RA Hirschfield A.N., Tilly J.L.;  
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and  
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal  
 RT endonuclease activity from morphological apoptosis in granulosa cells  
 RT of the ovarian follicle.";  
 RL Endocrinology 136:5042-5053 (1995).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97184204; PubMed=9030616;  
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rokey P.K.,  
 RA Rostek P. Jr., Poirier G.G., Paul S.M.;  
 RT "Cloning and expression of a rat brain interleukin-1beta-converting  
 RT enzyme (ICE)-related protease (IRP) and its possible role in  
 RT apoptosis of cultured cerebellar granule neurons.";  
 RL J. Neurosci. 17:1561-1569 (1997).  
 RN [4]  
 RN SEQUENCE OF 1-264 FROM N.A.  
 RA Yakovlev A.G.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
 CC 216-ASP-|-GLY-217 BOND. CLEAVES AND ACTIVATES STEROID REGULATORY  
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-  
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE  
 CC BUT NOT IN KIDNEY OR TESTIS.  
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS  
 CC OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE  
 CC ADULT BRAIN.  
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE  
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
 CC PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-7 PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND  
 CC VICE VERSA (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -----  
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 CC -----  
 CC EMBL: U49930; AAC52765.1; -  
 CC EMBL: U34685; AAC52261.1; -  
 CC EMBL: U84410; AAB41792.1; -  
 CC EMBL: U58456; AAB02722.1; -  
 CC HSSP: P42574; 1PAU.  
 CC MEROPS: C14.003; -  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR PRINTS: PR00376; IL1BCENZME.  
 DR SMART: SM00115; CASC; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.

DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.  
 FT PROPER 1 9  
 FT PROPER 10 28 BY SIMILARITY.  
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.  
 FT ACT\_SITE 121 121 APOPAIN P12 SUBUNIT.  
 FT ACT\_SITE 163 163 BY SIMILARITY.  
 FT CONFLICT 25 29 KSMDS -> QVD (IN REF. 4).  
 FT CONFLICT 170 170 C -> S (IN REF. 2).  
 FT CONFLICT 178 178 T -> A (IN REF. 2).  
 FT CONFLICT 182 182 M -> V (IN REF. 2).  
 FT CONFLICT 187 187 I -> K (IN REF. 2).  
 FT CONFLICT 190 190 E -> G (IN REF. 3).  
 FT CONFLICT 199 199 T -> S (IN REF. 2).  
 FT CONFLICT 211 211 D -> G (IN REF. 2).  
 FT CONFLICT 236 236 L -> I (IN REF. 4).  
 FT CONFLICT 245 245 T -> M (IN REF. 3).  
 SQ SEQUENCE 277 AA; 31491 MW; ADABFA18E2507402 CRC64;

Query Match 22.6%; Score 279.5; DB 1; Length 277;  
 Best Local Similarity 32.8%; Pred. No. 1.3e-15;  
 Matches 82; Conservative 35; Mismatches 106; Indels 27; Gaps 8;

QY 9 BEKYMGSAALILICVT-----KARGSEEDLDALHMFROLFESTMKRDP7A 58  
 DB 34 DSSYMDPDKMLCTIINKNPKHKTGMSARNGTDVDAANLAFETMALKYEVRRNKDIL7R 93  
 QY 59 EQFOEELKFOQAIIDREDPVSCAFVLMAGREGFLKGEDEMYKLEMLFEALNNKQ 118  
 DB 94 BEIMELMDSVSKEDSKSSKSSFCV---VILSHGDEGVIFGTNGP-VDLKCLTGFPGDYCR 149  
 QY 119 ALRARKYIIIIACGEGQDRPG-ETVSGDEITVMVTKDSQITPTTDAHVSTVEGYIA 177  
 DB 150 SLTGPKKFLIIQACRGTELDGCIETDSTGTDMMAC---QKIPVENDFLVAYSTAPGYYS 205  
 QY 178 YRHDKGSCFIOTLVDFYFKRGHILE---LLEVTYRMA---EAEVLQEGKARKTNP 230  
 DB 206 WRNSDGSFIIQSLC-AMKLVAHKLIEFMHILTRVNRKVAATEFESFLDATPAKQIDPC 264  
 QY 231 IOSTLRKRLY 240  
 DB 265 IYVSLTKELY 274

RESULT 7  
 ICE3\_CRILO STANDARD; PRT; 277 AA.  
 ID ICE3\_CRILO  
 AC 060431;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE APOPAIN precursor (BC 3.4.22.-) (Cysteine protease CPP32) (Yama  
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)  
 DE (SCA-1).  
 GN CASP3 OR CPP32.  
 OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCBI\_TaxId=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RC MEDLINE=96183185; PubMed=8605870;  
 RA Wang X., Zelenksi N.G., Yang J., Sakai J., Brown M.S.,  
 RA Goldstein J.L.;  
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by  
 RT CPP32 during apoptosis";  
 RL EMBL J. 15:1012-1020(1996).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
 CC PROTOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
 CC 216-ASP-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATOR  
 CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-  
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).  
 CC SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE  
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
 CC CASPASE-7. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-6 (BY SIMILARITY) AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND  
 CC VICE VERSA (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

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 CC -----  
 CC EMBL; U27463; AAB01511.1; -.  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.003; -.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; ILIACENZME.  
 DR SMART; SMO0115; CASC; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.  
 FT PROPER 1 9  
 FT PROPER 10 28 BY SIMILARITY.  
 FT CHAIN 29 175 APOPAIN P17 SUBUNIT.  
 FT ACT\_SITE 121 121 APOPAIN P12 SUBUNIT.  
 FT ACT\_SITE 163 163 BY SIMILARITY.  
 SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 22.4%; Score 277.5; DB 1; Length 277;  
 Best Local Similarity 35.9%; Pred. No. 1.8e-15;  
 Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

QY 29 REGSEEDLDALHMFROLFESTMKRDP7AFOEELKFOQAIIDREDPVSCAFVLM 88  
 DB 64 RSGTVDARKEFTFMALKYEVRRNKDILREIVELMKNASDEHSKSSFCV---VILS 120  
 QY 89 HREGFLKGEDEMYKLEMLFEALNNKQALRARKYIIIIACGEGQDRPG-ETVSGDE 147  
 DB 121 HDDEVITGTDP-IDLKLTISYFRGDCRSILGPKFLIIQACRGTELDGCIETDSTGE 179  
 QY 148 IVMVTKDSQITPTTDAHVSTVEGYIAVRHDKGSCFIOTLVDFYFKRGHILE--- 204  
 DB 180 DDMTC---QKIPVENDFLVAYSTAPGYYSNRNPNPDGSGWFIQSLCML-KVAHKLIEFMH 234  
 QY 205 LLEVTYRMA---EAEVLQEGKARKTNPETQSTLRKRLY 240  
 DB 235 ILTRVNRKVAATEFESFLDSTFPAKQIDPCIVSMLEKELY 274

RESULT 8  
 ICE3\_MOUSE STANDARD; PRT; 277 AA.  
 ID ICE3\_MOUSE  
 AC P70677; 008668;



RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).  
 RC TISSUE=T-cell;  
 RX MEDLINE=95074098; PubMed=7983002;  
 RA "Fernandes-Alnemri T., Litwack G., Alnemri E.S.;  
 RT "CPP32, a novel human apoptotic protein with homology to  
 RT Caenorhabditis elegans cell death protein Ced-3 and mammalian  
 RT interleukin-1 beta-converting enzyme.";  
 RL J. Biol. Chem. 269:30761-30764 (1994).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95292347; PubMed=7774019;  
 RA "Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,  
 RA Beutler D.R., Polver G.G., Salvesen G.S., Dixit V.M.;  
 RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable  
 RT protease that cleaves the death substrate poly(ADP-ribose)  
 RT polymerase.";  
 RL Cell 81:801-809 (1995).  
 RN [13]  
 RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.  
 RX MEDLINE=95319529; PubMed=7596430;  
 RA Nicholson D.W., Ali A., Thornberry N.A., Vailancourt J.P., Ding C.K.,  
 RA Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik V.A.,  
 RA Munday N.A., Raju S.M., Smolton M.E., Yamin T.-T., Li V.L.,  
 RA Miller D.K.;  
 RT "Identification and inhibition of the ICE/CED-3 protease necessary  
 RT for mammalian apoptosis.";  
 RL Nature 376:37-43 (1995).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.  
 RX MEDLINE=96266352; PubMed=8673606;  
 RA Roconda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,  
 RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vailancourt J.P.,  
 RA Thornberry N.A., Becker J.W.;  
 RT "The three-dimensional structure of apopain/CPP32, a key mediator of  
 RT apoptosis.";  
 RL Nat. Struct. Biol. 3:619-625 (1996).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.  
 RX MEDLINE=97197830; PubMed=9045680;  
 RA Mitchell P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,  
 RA Priestle J.P., Tomasek K.J., Grutter M.G.;  
 RT "Structure of recombinant human CPP32 in complex with the  
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";  
 RL J. Biol. Chem. 272:6539-6547 (1997).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=20283632; PubMed=10821855;  
 RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,  
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,  
 RA Levy M.A., Demolfi W.E. Jr., Keller P.M., Tomasek T., Head M.S.,  
 RA Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,  
 RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,  
 RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;  
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7  
 RT inhibit apoptosis and maintain cell functionality.";  
 RL J. Biol. Chem. 275:16007-16014 (2000).  
 RN [17]  
 RP PROCESSING.  
 RX MEDLINE=9635383; PubMed=8755496;  
 RA "Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,  
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomasek K.J.,  
 RA Litwack G., Alnemri E.S.;  
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human  
 RT apoptotic cysteine protease containing two FADD-like domains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).  
 RN [18]  
 RP CLEAVAGE OF HUNTINGTIN.  
 RX MEDLINE=96331285; PubMed=8696339;  
 RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,  
 RA Graham R.K., Brown M., Kazemi-Esfarjani P., Thornberry N.A.,  
 RA Vailancourt J.P., Hayden M.R.;  
 RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,  
 RT is modulated by the polyglutamine tract.";

RL Nat. Genet. 13:442-449 (1996).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
 CC PROTOLOGICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROID REGULATOR  
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-  
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE  
 CC CLEAVAGE OF HUNTINGTIN.  
 CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.  
 CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER  
 CC AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW  
 CC IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN  
 CC CELLS OF THE IMMUNE SYSTEM.  
 CC -1- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10  
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE  
 CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE  
 CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT  
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR  
 CC AND VICE VERSA.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U13737; AAA65015.1; -  
 CC EMBL: U13738; AAB60355.1; -  
 CC EMBL: U26943; AAA74929.1; -  
 CC PDB: 1PAU; 07-JUL-97.  
 CC PDB: 1CP3; 24-DEC-97.  
 CC PDB: 1GFW; 23-JUN-00.  
 CC MEROPS: C14.003; -  
 CC GeneW: HGNC:1504; CASP3.  
 CC MIM: 600636; -  
 CC InterPro: IPR003398; ICE.  
 CC InterPro: IPR001338; ICE\_P10.  
 CC InterPro: IPR001309; ICE\_P20.  
 CC Pfam: PF00655; ICE\_P10; 1.  
 CC Pfam: PF00656; ICE\_P20; 1.  
 CC PRINTS: PR00376; ILBCENZYM.  
 CC SMART: SM00115; CASP; 1.  
 CC PROSITE: PS01122; CASPASE\_CYS; 1.  
 CC PROSITE: PS01121; CASPASE\_HIS; 1.  
 CC PROSITE: PS50207; CASPASE\_P10; 1.  
 CC PROSITE: PS50208; CASPASE\_P20; 1.  
 CC Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;  
 KW 3D-structure.  
 FT PROPEP 1 9  
 FT PROPEP 10 28  
 FT CHAIN 176 277  
 FT CHAIN 176 277  
 FT ACT\_SITE 121 121  
 FT ACT\_SITE 163 163  
 FT VARIANT 190 190  
 FT /FTID=VAR\_001401.  
 SQ SEQUENCE 277 AA; 31594 MW; 8634DD2ACE6EF64B CRC64;  
 Query Match 22.0%; Score 272.5; DB 1; Length 277;  
 Best Local Similarity 31.9%; Pred. No. 4.6e-15;  
 Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;  
 QY 9 EEKYMGAALALILICVKK-----AREGSEEDLDALEHMFROLPFSTMTKRDPTA 58  
 DB 34 DNSTYMDYDPENGLCIILNNKNFKHSTGMTSAGTIVDANLRETRNLKYEVRANKNDLIR 93  
 QY 59 EGFQEELEKFOAIDSRDPSCAFVILMAHGREGLKGEDG--EMVKLENLEALNNKN 116

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Db 94 BEIYELMRDVSKEPHSKSSKSVFC---VLISHGEGIIFGTNGPVDLKKITNF---RGDR 147
Oy 117 COALRAKPKVYIIACRGEORDPG-ETVSGDEIYVWIKDSQTIPTYDALHYVTEGY 175
Db 148 CRSLTGRPKFTIACRGTETLDCGLETDSGVDDMAC---HKLPVADFLYAVSTARGY 203
Oy 176 IAYRHDKGSCFIOTLVDFVTK--RKGHILELTVETFRMA-EAEIVQ---EGKARKTP 229
Db 204 YSMNNSDGSFIIOSLCMLKQYADKLEFPHILTRVNRKVKATFEFSFDFATFPAKQIP 263
Oy 230 EIOSTLRKRLY 240
Db 264 CIVSMILTKELY 274

RESULT 10
ICE7_MOUSE STANDARD; PRT; 303 AA.
ID ICE7_MOUSE
AC P97864; O08669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Mortmainin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,
RA van Ioo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CASCADE AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION
CC PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF

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CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC -----
DR EMBL; U67321; AAC53068.1; ALT_INIT.
DR EMBL; D66353; BAA19730.1; -.
DR EMBL; Y13088; CAA73530.1; -.
DR EMBL; BC005428; AAH05428.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.004; -.
DR MGD; MGI:109383; Casp7.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM0115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR KX HydroLase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23 BY SIMILARITY.
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
FT ACT SITE 144 144 BY SIMILARITY.
FT ACT SITE 186 186 BY SIMILARITY.
FT CONFLICT 10 11 EL -> DW (IN REF. 2).
FT CONFLICT 45 45 A -> T (IN REF. 2).
FT CONFLICT 48 49 VR -> RQ (IN REF. 2).
SQ SEQUENCE 303 AA; 34060 MW; 747787B5BDE5F744 CRC64;

Query Match 21.8%; Score 270; DB 1; Length 303;
Best Local Similarity 32.6%; Pred. No. 8,3e-15;
Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;

Oy 29 REGSEEDLALHEHMFRLRFESTWKRDPYAFQGELEKFOQALDSREDPVSCAFVVLMA 88
Db 87 RNGTHDKDAGALFKCFQNLGFEVTHVNDSCAKMDDLKRSASEDHNS---ACFACVLIS 143
Oy 89 HGRGFLKGEDEGVKLENLEALNNKQALRAKPKVYIIACRGEORDPGRTVGDEI 148
Db 144 HGEEDLLYGDG-VTPKIDLTANFRGRCKTLLEKPLFTIQACRGTELDGIGQADSGPI 202
Oy 149 VMVVKDSQPTIPTYTDALHYVSTVEGYIAYRHDKGSCFIOTLVDFVTK--RKGHILEL 206
Db 203 NDIANPRNKIPVEADLPAVSTVPGYVSWNRNKGSGMPQALCSILNENKDELEIQIL 262
Oy 207 TEVTRMAEAEIVQEGAR---KTNPFIQSTLRKRLY 240
Db 263 TRVNDVRAHFESQSDPFRNEKQIPCMVSMILTKELY 300

RESULT 11
ICE7_MESAU STANDARD; PRT; 303 AA.
ID ICE7_MESAU
AC P55214;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-1-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
DE (SCA-2).

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GN CASP7 OR MCH3.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 ON NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=Syrian; TISSUE=Liver;  
 RX MEDLINE=96224303; PubMed=8643593;  
 RA Pal U.-T., Brown W.S., Goldstein J.L.;  
 RT "Purification and cDNA cloning of a second apoptosis-related cysteine  
 RT protease that cleaves and activates sterol regulatory element binding  
 RT proteins";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).  
 CC  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL  
 CC REGULATORY ELEMENT BINDING PROTEINS (SREBPs). PROTEOLYTICALLY  
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217  
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY  
 CC SIMILARITY).  
 CC  
 CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT  
 CC (BY SIMILARITY).  
 CC  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC  
 CC -1- PTM: CLEAVAGES BY GRANTZME B OR CASPASE-10 GENERATE THE TWO ACTIVE  
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY  
 CC CPP32. PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND  
 CC VICE VERSA (BY SIMILARITY).  
 CC  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC  
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 CC  
 CC -----  
 CC EMBL: U47332; AAC52595.1; -;  
 CC HSSP: P42574; IPAU.  
 CC  
 CC DR MEROPS: C14.004; -;  
 CC DR InterPro: IPR002398; ICE.  
 CC DR InterPro: IPR002138; ICE\_P10.  
 CC DR InterPro: IPR001309; ICE\_P20.  
 CC  
 CC DR Pfam: PF00655; ICE\_P10; 1.  
 CC DR Pfam: PF00656; ICE\_P20; 1.  
 CC DR PRINTS: PR00376; ILHICENZYM.  
 CC DR SMART: SM00115; CASC; 1.  
 CC  
 CC DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 CC DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 CC DR PROSITE: PS50207; CASPASE\_P10; 1.  
 CC DR PROSITE: PS50208; CASPASE\_P20; 1.  
 CC  
 CC KW Hydrolase; Thiol protease; Zymogen; Apoptosis.  
 CC  
 CC FT CHAIN 1 23  
 CC FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.  
 CC FT PROPEP 199 206 BY SIMILARITY.  
 CC FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.  
 CC FT ACT\_SITE 144 144 BY SIMILARITY.  
 CC FT ACT\_SITE 186 186 BY SIMILARITY.  
 CC SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;  
 CC  
 CC Query Match 21.0%; Score 260; DB 1; Length 303;  
 CC Best Local Similarity 31.7%; Pred. No. 5.3e-14;  
 CC Matches 69; Conservative 39; Mismatches 100; Indels 10; Gaps 5;

QY 149 VMVIXDSPQITPTVTDALHYSTVEGYIAYRHDKGSCFIQTLVDVETK--RKGHILELL 206  
 Db 203 NETDANRPRYKIPVADFLFVAVSTVGYSWRNPKGSMFQALCSIDHKGKLEIMQIL 262  
 QY 207 TEVTRRNA--EAEVDE-GKARTNPEIOSTLARKLY 240  
 Db 263 TRVNDRAVRHRESOCDDPCFNEKKOIPCMWSMLTKELY 300  
 RESULT 12  
 ID C77\_HUMAN STANDARD; PRT; 303 AA.  
 AC P55210; Q13364; Q96BA0;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-7 precursor (BC 3.4.22.-) (ICE-like apoptotic protease 3)  
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (CWH-1).  
 GN CASP7 OR MCH3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ALPHA ISOFORM).  
 RX MEDLINE=96139498; PubMed=8576161;  
 RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,  
 RA Dixit V.M.;  
 RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans  
 RT cell death protein Ced-3, is activated during Fas- and tumor necrosis  
 RT factor-induced apoptosis";  
 RL J. Biol. Chem. 271:1621-1625(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ALPHA ISOFORM).  
 RX TISSUE=Spleen;  
 RC MEDLINE=96147144; PubMed=8567622;  
 RA Lipke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;  
 RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel  
 RT cysteine protease similar to CPP32";  
 RL J. Biol. Chem. 271:1825-1828(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).  
 RC TISSUE=T-cell;  
 RX MEDLINE=96105019; PubMed=8521391;  
 RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,  
 RA Fritz L.C., Tomaselli K.J., Wang L., Xu Z., Croce C.M., Salveson G.,  
 RA Earnshaw W.C., Litwack G., Alnemri E.S.;  
 RT "Mch3, a novel human apoptotic cysteine protease highly related to  
 RT CPP32";  
 RL Cancer Res. 55:6045-6052(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS).  
 RC TISSUE=Fetal lung, and Fetal spleen;  
 RX MEDLINE=97224489; PubMed=9070923;  
 RA Juan T.S.-C., McViee I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., Fletcher P.A.;  
 RT "Identification and mapping of Casp7, a cysteine protease resembling  
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3";  
 RL Genomics 40:86-93(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ALPHA ISOFORM).  
 RC TISSUE=Skin;  
 RA Strauberg R.;  
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP PROCESSING.  
 RX MEDLINE=9635838; PubMed=8755496;  
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,  
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,  
 RA Litwack G., Alnemri E.S.;  
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human  
 RT apoptotic cysteine protease containing two FAD-like domains";

RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).

CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL

CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY

CC CLEAVES POLY (ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-GLY-217

CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.

CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.

CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (p20) AND A 11 kDa (p11) SUBUNIT.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS. ALPHA (SHOWN HERE), BETA AND

CC ALPHA'; ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM IS

CC NOT PROTEOLYTICALLY ACTIVE.

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,

CC LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO

CC EXPRESSION IN THE BRAIN.

CC -1- PFM: CLEAVAGES BY GRANTZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE

CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY

CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF

CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND

CC VICE VERSA.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

CC -1- CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4 AS BETA,

CC BUT AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED IT ALPHA'.

CC -----

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CC -----

DR EMBL: U39613; AAC50346.1; -

DR EMBL: U40281; AAC50352.1; -

DR EMBL: U37448; AAC50303.1; -

DR EMBL: U37449; AAC50304.1; -

DR EMBL: U67319; AAC51152.1; -

DR EMBL: U67320; AAC51153.1; -

DR EMBL: U67206; AAF21460.1; -

DR EMBL: BC015799; AAH15799.1; -

DR HSSP: P43574; 1PAU.

DR MEROPS: C14.004; -

DR Genew; HGNC:1508; CASP7.

DR MIM; 601761; -

DR Interpro: IPR002398; ICE.

DR Interpro: IPR002138; ICE\_p10.

DR Interpro: IPR001309; ICE\_p20.

DR Pfam; PF00655; ICE\_p10.1.

DR Pfam; PF00656; ICE\_p20.1.

DR PRINTS; PR00376; IL1BCENZME.

DR SMART; SMO0115; CASC; 1.

DR PROSITE; PS01123; CASPASE\_CYS; 1.

DR PROSITE; PS01121; CASPASE\_HIS; 1.

DR PROSITE; PS50207; CASPASE\_P10; 1.

DR PROSITE; PS50208; CASPASE\_P20; 1.

DR Hydrobase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.

FT PROPEP 1 23

FT CHAIN 24 198

FT PROPEP 199 206

FT CHAIN 207 303

FT ACT\_SITE 144 144

FT ACT\_SITE 186 186

FT VARSPIC 1 1

FT VARSPIC 149 303

FT VARSPIC 149 303

M -> MDCVMPGRKKHLEKNTSCGSSGSCASYVMQ

(IN ISOFORM ALPHA').

VIVGKDVTPKIDTAHFRGRCRCKTLLEKPLFTIQACRG

ELDGIQADSGPINDTANPRYKIPVADFLFAVSTVGY

SMRSPGSGWFWQALCSILIEHGKDLIMQILTVNDRVR

HFEESGDDPHFEKKQICVVSMTLKYLSQ -> MESS

VTOGVQRDGLGRIGPPRPLAEGSPALMASAPRGSSMO

MLIDTRSKOMLTSSSIPRFQATTRGAGAEARGLKPSA

PSMSTKTKMSCKSSPG (IN ISOFORM BETA).

C->A: NO APOPTOTIC ACTIVITY.

D -> E (IN REF. 5).

FT CONFLICT 194 194 G -> A (IN REF. 1).

SO SEQUENCE 303 AA; 34276 MW; CD373EE54A232C44 CRC64;

Query Match 20.7%; Score 256; DB 1; Length 303;

Best Local Similarity 30.7%; Pred. No. 1.1e-13;

Matches 67; Conservative 39; Mismatches 102; Indels 10; Gaps 4;

Oy 29 REGSEEDLDLLEHMFRLPRESTTKRDPRTAEQFOELEKFOALDSREDPVSCAFVYLM 88

Db 87 RINGDKDAEALFKFRSLGFDVLYVNDSCAKQDILK--ASEEDHTNACFACILLS 143

Oy 89 HGREFLKGEDEWVLENTPEALNNKNCALRAKPVYI11QACGEORDPGEFTVGDEI 148

Db 144 HGEENVIVYGDG-VTPKIDTAHFRGRCRCKTLLEKPLFTIQACRGTELDG1QADSGPI 202

Oy 149 VMVTKDSPPQIPPTDNLHYSTEGYIARHNDKSCSFQTLVDVFTK--RKHILIEL 206

Db 203 NDTNANPRYKIPVEADFLFAVSTVPGYVSWRSPGSGWFWQALCSILIEHGKDLIMQIL 262

Oy 207 TEVTRMAEALVQEG---KARKTNPEIQSTLRKRLY 240

Db 263 TRVNDVRAHFEESGDDPHFEKKQICVVSMTLKYLY 300

RESULT 13

CEB3\_CABEL STANDARD; PRT; 503 AA.

AC P42573; P45435; Q9YAO8;

DT 01-NOV-1995 (Rel. 32, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cell death protein 3 precursor (EC 3.4.22.-).

GN CED-3 OR C48D1.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;

OC Rhabditidae; Pelodertinae; Caenorhabditis.

OC NCBI Taxid=6239;

RP [1]

RP SEQUENCE FROM N.A. AND MUTAGENESIS.

RC STRAIN=Bristol N2;

RA MEDLINE=94061982; PubMed=8242740;

RA Yuan J., Shaham S., Jedoux S., Ellis H.M., Horvitz H.R.;

RT "The C. elegans cell death gene ced-3 encodes a protein similar to

RL Celi 75:641-652(1993).

RN [2]

RN REVISION TO 418.

RA Horvitz H.R.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Burton J.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP REVISIONS.

RA Durbin R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ACTS AS A CYSTEINE PROTEASE IN CONTROLLING PROGRAMMED

CC CELL DEATH BY PROTEOLYTICALLY ACTIVATING OR INACTIVATING A

CC SUBSTRATE PROTEIN OR PROTEINS. A POTENTIAL SUBSTRATE MAY BE CED-4.

CC ALTERNATIVELY IT MIGHT DIRECTLY CAUSE CELL DEATH BY

CC PROTEOLYTICALLY CLEAVING PROTEINS THAT ARE CRUCIAL FOR CELL

CC VIABILITY.

CC -1- SUBUNIT: COULD BE A HETERODIMER OF TWO SUBUNITS DERIVED FROM THE

CC PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM.

CC -1- DEVELOPMENTAL STAGE: MOST ABUNDANT DURING EMBRYOGENESIS AND IS

CC ALSO DETECTED AT LATER STAGES.

CC -1- PFM: MAY BE REGULATED BY PHOSPHORYLATION.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.

CC -----

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DR EMBL: Y12261; CA72937.1; -  
 DR EMBL: AE003771; AAF56939.1; -  
 DR HSSP: P42574; 1PAU.  
 DR MEROPS: C14.015; -  
 DR FlyBase: Fgn00019972; Ice.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_P10.  
 DR InterPro: IPR001309; ICE\_P20.  
 DR Pfam: PF00655; ICE\_P10; 1.  
 DR Pfam: PF00656; ICE\_P20; 1.  
 DR PRINTS: PR00376; ILICENZYME.  
 DR SMART: SM00115; CASc; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.  
 FT PROPEP 1 28 BY SIMILARITY.  
 FT CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).  
 FT PROPEP 218 230 BY SIMILARITY.  
 FT CHAIN 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).  
 FT ACT SITE 169 169 BY SIMILARITY.  
 FT ACT SITE 211 211 BY SIMILARITY.  
 FT CONFLICT 151 151 A -> S (IN REF. 1).  
 FT CONFLICT 265 265 S -> T (IN REF. 1).  
 FT SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;

Query Match 20.0%; Score 247.5; DB 1; Length 339;  
 Best Local Similarity 30.5%; Pred. No. 6,3e-13;  
 Matches 60; Conservative 42; Mismatches 76; Indels 19; Gaps 5;

QY 27 KAREGEEDLDALHEMRQRLFEESTMKRDPFAEQFOELEKFGQALDSREDPVSQAFVL 86  
 DB 110 KSRAGTIVDCENLTRVLKQJLDFEVTYKDC--RYKDLRTIEVYAAQSNHSDSCILVAI 166  
 QY 87 MAHGREFLKGEDEMKLENTFEALNNKNGQALRAKPKVYIIAGCGEQDPRETV--- 143  
 DB 167 LSHGEWYIYAKDTQ-YKLDNWSFPTANHCPSLAGRKPLFFIACQCDRLDGGVTMORS 225  
 QY 144 ----GGDEIYVWIKDSPTIPTYTDALHVSTEGYIAYRHDKSGCFIOTLVVFTK-- 197  
 DB 226 QTEWDG-----SSMKYKIPVADFLIAYSTVDFGFSMRTTNGSMFMQSLCAELANG 279  
 QY 198 RKGHLELLEVTERRMA 214  
 DB 280 KRDLITLLTFVCCORVA 296

RESULT 15  
 ICE8\_HUMAN STANDARD; PRT; 479 AA.  
 ID ICE8\_HUMAN STANDARD; PRT; 479 AA.  
 AC Q14750; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;  
 AC Q15806; Q9U081; Q14676;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)  
 DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-  
 DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)  
 DE (Apoptotic protease Mch-5) (CASP4).  
 GN CASP8 OR MCH5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Thymus, and B-cell;

RX MEDLINE=96279826; PubMed=8681376;  
 RA Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D.,  
 RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in  
 RT Fas/APO-1- and TNF receptor-induced cell death";  
 RL Cell 85:803-815(1996).  
 RN [12]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=96279827; PubMed=8681377;  
 RA Muzio M., Chinaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,  
 RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,  
 RA Kramer P.H., Peter M.E., Dixit V.M.,  
 RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited  
 RT to the CD95 (Fas/APO-1) death-inducing signaling complex";  
 RL Cell 85:817-827(1996).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RX MEDLINE=96353838; PubMed=8755496;  
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,  
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,  
 RA Litwack G., Alnemri E.S.,  
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human  
 RT apoptotic cysteine protease containing two FADD-like domains";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99132295; PubMed=9931493;  
 RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.,  
 RT "Structure and chromosome localization of the human CASP8 gene";  
 RL Gene 226:225-232(1999).  
 RN [15]  
 RP SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).  
 RX MEDLINE=97373543; PubMed=9228018;  
 RA Srinivasula S.M., Ahmed M., Oltie S., Bullrich F., Banks S.,  
 RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomaselli K.J.,  
 RA Armstrong R.C., Alnemri E.S.,  
 RT "FLAME-1, a novel FADD-like anti-apoptotic molecule that regulates  
 RT Fas/TNFR1-induced apoptosis";  
 RL J. Biol. Chem. 272:18542-18545(1997).  
 RN [16]  
 RP PARTIAL SEQUENCE, AND PROCESSING.  
 RX MEDLINE=97121412; PubMed=8962078;  
 RA Srinivasula S.M., Ahmed M., Fernandes-Alnemri T., Litwack G.,  
 RA Alnemri E.S.,  
 RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1  
 RT Ced-3/ICE-like cysteine proteases";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).  
 RN [17]  
 RP FUNCTION.  
 RX MEDLINE=97160607; PubMed=9006941;  
 RA Muzio M., Salvesen G.S., Dixit V.M.,  
 RT "FLICE induced apoptosis in a cell-free system. Cleavage of caspase  
 RT zymogens";  
 RL J. Biol. Chem. 272:2952-2956(1997).  
 RN [18]  
 RP PROCESSING.  
 RX MEDLINE=97327557; PubMed=9184224;  
 RA Medina J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,  
 RA Kramer P.H., Peter M.E.,  
 RT "FLICE is activated by association with the CD95 death-inducing  
 RT signaling complex (DISC)";  
 RL EMBO J. 16:2794-2804(1997).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=99451259; PubMed=10508784;  
 RA Blanchard H., Kodandapani L., Mitali P.R.E., Di Marco S., Krebs J.F.,  
 RA Wu J.C., Tomaselli K.J., Grueter M.G.,  
 RT "The three-dimensional structure of caspase-8: an initiator enzyme in  
 RT apoptosis";  
 RL Structure 7:1125-1133(1999).  
 CC -!- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF  
 CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND

CC TNFR-1 INDUCED CELL DEATH: BINDING TO THE ADAPTOR MOLECULE FADD  
 CC RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED  
 CC THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH  
 CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN  
 CC LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC  
 CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE  
 CC (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC.  
 CC CLEAVES AND ACTIVATES CASPASE-3, -4, -6, -7, -9, AND -10. MAY  
 CC PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY  
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYZES THE SMALL-  
 CC MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-|-AMC. LIKELY TARGET FOR  
 CC THE COMPLEX VIRUS CRMA DEATH INHIBITORY PROTEIN.  
 CC SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 10 kDa (P10) SUBUNIT.  
 CC INTERACTS WITH CFLAR.  
 CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1-ALPHA (SHOWN HERE), 2-  
 CC ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-  
 CC BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE EXPRESSED IN A  
 CC WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIPHERAL BLOOD  
 CC LEUKOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECTABLE IN BRAIN,  
 CC TESTIS, AND SKELETAL MUSCLE.  
 CC -1- PM: GENERATION OF THE SUBUNIT REQUIRES ASSOCIATION WITH THE  
 CC DISC, WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE  
 CC AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND  
 CC CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).  
 CC -----  
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 CC -----  
 DR EMBL; X98172; CAA66853.1; -;  
 DR EMBL; X98173; CAA66854.1; -;  
 DR EMBL; X98174; CAA66855.1; -;  
 DR EMBL; X98175; CAA66856.1; -;  
 DR EMBL; X98176; CAA66857.1; -;  
 DR EMBL; X98177; CAA66858.1; -;  
 DR EMBL; X98178; CAA66859.1; -;  
 DR EMBL; U58143; AAC50602.1; -;  
 DR EMBL; U60520; AAC50645.1; -;  
 DR EMBL; AF102146; AAD24962.1; -;  
 DR EMBL; AF102139; AAD24962.1; JOINED.  
 DR EMBL; AF102140; AAD24962.1; JOINED.  
 DR EMBL; AF102141; AAD24962.1; JOINED.  
 DR EMBL; AF102142; AAD24962.1; JOINED.  
 DR EMBL; AF102143; AAD24962.1; JOINED.  
 DR EMBL; AF102144; AAD24962.1; JOINED.  
 DR EMBL; AF102145; AAD24962.1; JOINED.  
 DR EMBL; AF1009620; AAB70913.1; -;  
 DR PDB; 1ODU; 10-JUL-00.  
 DR MEROPS; C14.009; -;  
 DR GeneW; HGNC:1509; CASP8.  
 DR MIM; 601763; -;  
 DR InterPro; IPR001875; DED.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR Pfam; PF01335; DED; 2.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 DR PROSITE; PS50168; DED; 2.  
 KM Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing;  
 KW Repeat; 3d-structure.  
 FT PROPEP 1 216  
 FT CHAIN 217 374 CASPASE-8 SUBUNIT P18.

FT PROPEP 375 384  
 FT CHAIN 385 479  
 FT ACT\_SITE 317 317  
 FT ACT\_SITE 360 360  
 FT DOMAIN 2 80  
 FT DOMAIN 100 177  
 FT VARSPPLIC 102 102  
 FT VARSPPLIC 184 198  
 FT VARSPPLIC 184 220  
 FT VARSPPLIC 184 267  
 FT VARSPPLIC 199 235  
 FT VARSPPLIC 221 479  
 FT VARSPPLIC 236 479  
 FT VARSPPLIC 269 276  
 FT VARSPPLIC 277 479  
 FT CONFLICT 285 285  
 FT CONFLICT 294 294  
 FT CONFLICT 331 331  
 FT SEQUENCE 479 AA; 55391 MW; 7A5FEADA6B39B582F CRC64;  
 SQ  
 Query Match 19.9%; Score 246.5; DB 1; Length 479;  
 Best Local Similarity 29.7%; Pred. No. 1.2e-12;  
 Matches 80; Conservative 37; Mismatches 115; Indels 37; Gaps 9;  
 QY 3 NPRSLEEK-----YDMSGALALILCV-----TKARE-----GSEEDLDAL 39  
 DB 211 SPREDSSQTLDKYQKSKRGVCLINNHPKAREKXPXKHSIRDRNGTHDAQAL 270  
 QY 40 EHMFRQLRPESTMTRKDPFAEQFOEELKFPQALDSREDPSCAFVLMAGREGFLKED 99  
 DB 271 TTFPELHFELKPHDDCTVEQIYEILKIQQLMDHSHNM-----CFICCLISHGDKGIYGTD 327  
 QY 100 GEMVLENTLFEALNNKCOALRAKPKYVILIOACRGEQCDPBEVSGD-----IYVWIDS 155  
 DB 328 GQEADIVELTSGTGLKCPSLAGKPKVFPIQACQSDNYQKGIPIETDSEBOPYLEMDLSS 387  
 QY 156 POT--IPTYDALHYSTVEGYIAYRHQKSGSCFIQTLVDVFTKR--XG-HILELLEVT 210  
 DB 368 POTRIIPDEADPLLGMAIVNNCVSYRNPABGTWYIQLCSLRRCRPGDILTLITLVN 447  
 QY 211 RMAEAEIVQEGKARKNPEIQSTLRKL 239  
 DB 448 YEVSXND--DKKMGKQMPQPTFLRKL 474

Search completed: February 26, 2003, 12:19:26  
 Job time : 9.19522 secs

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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:20:36 ; Search time 9.64143 Seconds  
(without alignments)  
946.818 Million cell updates/sec

Title: US-09-989-903-5  
Sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKTPEIQTSLRKLYIQ 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174566 seqs, 37721826 residues  
Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB pep:\*
  - 2: /cgn2\_6/ptodata/2/pubppaa/PTCT\_NEW\_PUB pep:\*
  - 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB pep:\*
  - 4: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB pep:\*
  - 5: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB pep:\*
  - 6: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB pep:\*
  - 7: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB pep:\*
  - 8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB pep:\*
  - 9: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB pep:\*
  - 10: /cgn2\_6/ptodata/2/pubppaa/US05\_PUBCOMB pep:\*
  - 11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB pep:\*
  - 12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB pep:\*
  - 13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB pep:\*
  - 14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	242	10	US-09-989-903-5
2	1234	99.6	242	10	US-09-945-028-2
3	1194	96.4	242	10	US-09-764-803A-24
4	1189	96.0	242	10	US-09-845-028-9
5	1166	94.1	229	10	US-09-764-803A-4
6	1065	86.0	214	10	US-09-989-903-9
7	934.5	75.4	257	10	US-09-764-803A-2
8	934.5	75.4	260	10	US-09-989-903-2
9	890	71.8	230	10	US-09-989-903-7
10	295	23.8	451	10	US-09-888-243-28
11	293	23.6	74	10	US-09-989-903-63
12	289	23.3	435	10	US-09-954-697-9
13	273.5	22.1	277	10	US-09-895-263-4
14	272.5	22.0	264	9	US-10-103-448-3
15	272.5	22.0	264	9	US-10-108-929-3
16	272.5	22.0	277	10	US-09-954-697-12
17	256	20.7	303	10	US-09-944-851-2
18	256	20.7	303	10	US-09-954-697-24
19	252	20.3	303	10	US-09-895-263-2

20	251	20.3	505	10	US-09-888-243-5	Sequence 5, Appl1
21	248	20.0	479	10	US-09-952-768-2	Sequence 2, Appl1
22	248	20.0	479	10	US-09-954-697-33	Sequence 33, Appl1
23	247.5	20.0	479	10	US-09-888-243-6	Sequence 6, Appl1
24	247.5	20.0	466	10	US-09-952-768-4	Sequence 4, Appl1
25	246.5	19.9	286	10	US-09-862-915-1	Sequence 1, Appl1
26	246.5	19.9	479	10	US-09-410-194-20	Sequence 20, Appl1
27	246	19.9	479	10	US-09-954-697-27	Sequence 27, Appl1
28	245.5	19.8	503	10	US-09-888-243-29	Sequence 29, Appl1
29	239.5	19.3	416	9	US-10-068-569-1	Sequence 1, Appl1
30	232.5	18.8	416	9	US-10-059-749-2	Sequence 2, Appl1
31	232.5	18.8	416	10	US-09-954-697-30	Sequence 30, Appl1
32	226	18.2	383	10	US-09-764-803A-23	Sequence 23, Appl1
33	226	18.2	404	9	US-09-827-708A-2	Sequence 2, Appl1
34	226	18.2	404	10	US-09-954-697-6	Sequence 6, Appl1
35	225	18.2	404	10	US-09-888-243-30	Sequence 10, Appl1
36	225	18.2	418	10	US-09-954-697-18	Sequence 18, Appl1
37	222	17.9	293	10	US-09-954-697-21	Sequence 21, Appl1
38	221.5	17.9	354	10	US-09-888-243-20	Sequence 20, Appl1
39	221.5	17.9	503	10	US-09-888-243-2	Sequence 2, Appl1
40	221.5	17.9	521	10	US-09-962-834A-2	Sequence 2, Appl1
41	221.5	17.9	571	10	US-09-410-194-21	Sequence 21, Appl1
42	217.5	17.6	402	10	US-09-888-243-14	Sequence 14, Appl1
43	214	17.3	293	9	US-10-171-077-5	Sequence 5, Appl1
44	211	17.0	410	10	US-09-917-265-24	Sequence 24, Appl1
45	210.5	17.0	410	10	US-09-917-265-15	Sequence 15, Appl1

ALIGNMENTS

RESULT 1  
US-09-989-903-5  
Sequence 5, Application US/09989903  
Patent No. US0020146804A1  
GENERAL INFORMATION:  
APPLICANT: Alnemati, Emdad S.  
TITLE OF INVENTION: Fernandez-Alnemati, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
FILE REFERENCE: 460140.434D1  
CURRENT APPLICATION NUMBER: US/09/989, 903  
CURRENT FILING DATE: 2002-04-11  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-989-903-5

Query Match 100.0%; Score 1239; DB 10; Length 242;  
Best Local Similarity 100.0%; Pred. No. 6.8e-113;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSNPRSLSEEEKYDMSGALALILCTYKARSGESDLDLLEHMPOLRRESTMKRPTAEQ 60	
DB	1	MSNPRSLSEEEKYDMSGALALILCTYKARSGESDLDLLEHMPOLRRESTMKRPTAEQ 60	
QY	61	FOEELKEFOAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVXLENLFEALNNKQCAL 120	
DB	61	FOEELKEFOAIDSRDPVSCAFVVLMAHGREGLKSGDEGMVXLENLFEALNNKQCAL 120	
QY	121	RAKPRVYIQCRCRQRPDGETVGDDELVMYIKSPQITPYTDALHYSTVEGIIAYRH 180	
DB	121	RAKPRVYIQCRCRQRPDGETVGDDELVMYIKSPQITPYTDALHYSTVEGIIAYRH 180	
QY	181	DOKSCFIQTLVDVFTTKKGIHLELTVTRMAEALVOGKARKTPEIQTSLRKLY 240	
DB	181	DOKSCFIQTLVDVFTTKKGIHLELTVTRMAEALVOGKARKTPEIQTSLRKLY 240	
QY	241	IQ 242	

Db 241 LQ 242

# RESULT 2

US-09-845-028-2  
 ; Sequence 2, Application US/09845028  
 ; Patent No. US20020081705A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mankovich, John  
 ; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS  
 ; FILE REFERENCE: BI-111  
 ; CURRENT APPLICATION NUMBER: US/09/845,028  
 ; CURRENT FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 60/199,962  
 ; PRIOR FILING DATE: 2000-04-27  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 242  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-845-028-2

Query Match 99.6%; Score 1234; DB 10; Length 242;  
 Best Local Similarity 99.6%; Pred. No. 2.1e-112;  
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEBDLDALEHMFROLRFESTMKRDPPTAQ 60  
 DB 1 MSNPRLSEEEKYDMSGARLALILCVTKAREGSEBDLDALEHMFROLRFESTMKRDPPTAQ 60  
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120  
 DB 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120  
 QY 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180  
 DB 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180  
 QY 181 DOKGSCFIQTLVDVFTKRGHILELLEVTTRMAEAEIVOEGKARKTNPEIOSTLRKRLY 240  
 DB 181 DOKGSCFIQTLVDVFTKRGHILELLEVTTRMAEAEIVOEGKARKTNPEIOSTLRKRLY 240  
 QY 241 LQ 242  
 DB 241 LQ 242

# RESULT 3

US-09-764-803A-24  
 ; Sequence 24, Application US/09764803A  
 ; Patent No. US20020034812A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Van de Craen, Marc  
 ; APPLICANT: Declercq, Wim  
 ; APPLICANT: Vandenaebiele, Peter  
 ; APPLICANT: Fiers, Walter  
 ; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE  
 ; FILE REFERENCE: 2676-4661US  
 ; CURRENT APPLICATION NUMBER: US/09/764,803A  
 ; CURRENT FILING DATE: 2001-01-17  
 ; PRIOR APPLICATION NUMBER: PCT/EP99/04939  
 ; PRIOR FILING DATE: 1999-07-12  
 ; PRIOR APPLICATION NUMBER: EP 9820242.6  
 ; PRIOR FILING DATE: 1999-07-17  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 24  
 ; LENGTH: 242  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature

; OTHER INFORMATION: Description of Artificial Sequence: predicted (genscan program) h  
 ; OTHER INFORMATION: uman caspase-1  
 ; US-09-764-803A-24

Query Match 96.4%; Score 1194; DB 10; Length 242;  
 Best Local Similarity 97.1%; Pred. No. 1.6e-108;  
 Matches 235; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKAREGSEBDLDALEHMFROLRFESTMKRDPPTAQ 60  
 DB 1 MNPRLSEEEKYDMSGARLALILCVTKAREGSEBDLDALEHMFROLRFESTMKRDPPTAQ 60  
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120  
 DB 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOAL 120  
 QY 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180  
 DB 121 RAKPKVYIIQACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRH 180  
 QY 181 DOKGSCFIQTLVDVFTKRGHILELLEVTTRMAEAEIVOEGKARKTNPEIOSTLRKRLY 240  
 DB 181 DOKGSCFIQTLVDVFTKRGHILELLEVTTRMAEAEIVOEGKARKTNPEIOSTLRKRLY 240  
 QY 241 LQ 242  
 DB 241 LQ 242

# RESULT 4

US-09-845-028-9  
 ; Sequence 9, Application US/09845028  
 ; Patent No. US20020081705A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mankovich, John  
 ; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS  
 ; FILE REFERENCE: BI-111  
 ; CURRENT APPLICATION NUMBER: US/09/845,028  
 ; CURRENT FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 60/199,962  
 ; PRIOR FILING DATE: 2000-04-27  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 242  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-845-028-9

Query Match 96.0%; Score 1189; DB 10; Length 242;  
 Best Local Similarity 99.6%; Pred. No. 4.9e-108;  
 Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 EKYDMSGALALILCVTKAREGSEBDLDALEHMFROLRFESTMKRDPPTAQFOEELKFO 69  
 DB 10 EKYDMSGARLALILCVTKAREGSEBDLDALEHMFROLRFESTMKRDPPTAQFOEELKFO 69  
 QY 70 QAIDSRREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOALRAKPKVYII 129  
 DB 70 QAIDSRREDPVSCAFVVLMAHGREGLKGEDEGVKLENLFEALNNKCOALRAKPKVYII 129  
 QY 130 QACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRHQKSCFIQ 189  
 DB 130 QACRGQRDPGETVSGDEIWMVKDSPTIPTYTDLAHVYSTVEGYIAYRHQKSCFIQ 189  
 QY 190 TLVDVFTKRGHILELLEVTTRMAEAEIVOEGKARKTNPEIOSTLRKRLYQ 242  
 DB 190 TLVDVFTKRGHILELLEVTTRMAEAEIVOEGKARKTNPEIOSTLRKRLYQ 242

# RESULT 5

US-09-764-803A-4  
 ; Sequence 4, Application US/09764803A

```

; Patent No. US20020034812A1
; GENERAL INFORMATION:
; APPLICANT: Van de Craen, Marc
; APPLICANT: Declercq, Wim
; APPLICANT: Vandenaebale, Peter
; APPLICANT: Fiers, Walter
; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
; FILE REFERENCE: 2676-466IUS
; CURRENT APPLICATION NUMBER: US/09/764, 803A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: PCT/EP99/04939
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EP 98202422.6
; PRIOR FILING DATE: 1999-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-803A-4

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Query Match 94.1%; Score 1166; DB 10; Length 229;
Best Local Similarity 99.6%; Pred. No. 7.8e-106;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 14 MSGAALLILCTVARESEEDLDALHMPROLRESTMKRDPPTAEQOELEKFOQAID 73
DB 1 MSGARLALILCTVARESEEDLDALHMPROLRESTMKRDPPTAEQOELEKFOQAID 60
QY 74 SREDPVSCAFVVLMAHGREGLKGEDGEMVLENLFEALNNKNCALRAKRVYIIQACR 133
DB 61 SREDPVSCAFVVLMAHGREGLKGEDGEMVLENLFEALNNKNCALRAKRVYIIQACR 120
QY 134 GEQDPEGTGDEIWMYIKDSPOTIPYTDALHYSTVEGIYARHDQKSCFIQTLVD 193
DB 121 GEQDPEGTGDEIWMYIKDSPOTIPYTDALHYSTVEGIYARHDQKSCFIQTLVD 180
QY 194 VFTKRKGHILELLEVTNRMAEALVOEGKARKTNPEIQTSLRKRLYLQ 242
DB 181 VFTKRKGHILELLEVTNRMAEALVOEGKARKTNPEIQTSLRKRLYLQ 229

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RESULT 6
US-09-989-903-9
; Sequence 9, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989, 903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-903-9

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Query Match 86.0%; Score 1065; DB 10; Length 214;
Best Local Similarity 88.0%; Pred. No. 4.6e-96;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

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QY 1 MSNPRSLSEEEKYDMSGALALILCTVARESEEDLDALHMPROLRESTMKRDPPTAEQ 60
DB 1 MSNPRSLSEEEKYDMSGALALILCTVARESEEDLDALHMPROLRESTMKRDPPTAEQ 34
QY 61 FOEELKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVLENLFEALNNKNCAL 120
DB 61 FOEELKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVLENLFEALNNKNCAL 120

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DB 35 --EELEKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVLENLFEALNNKNCAL 92
QY 121 RAKPKVYIIQACRGEQDPEGTGDEIWMYIKDSPOTIPYTDALHYSTVEGIYARH 180
DB 93 RAKPKVYIIQACRGEQDPEGTGDEIWMYIKDSPOTIPYTDALHYSTVEGIYARH 152
QY 181 DQKSCFIQTLVDVFTKRKGHILELLEVTNRMAEALVOEGKARKTNPEIQTSLRKRL 240
DB 153 DQKSCFIQTLVDVFTKRKGHILELLEVTNRMAEALVOEGKARKTNPEIQTSLRKRL 212
QY 241 LQ 242
DB 213 LQ 214

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RESULT 7
US-09-764-803A-2
; Sequence 2, Application US/09764803A
; Patent No. US20020034812A1
; GENERAL INFORMATION:
; APPLICANT: Van de Craen, Marc
; APPLICANT: Declercq, Wim
; APPLICANT: Vandenaebale, Peter
; APPLICANT: Fiers, Walter
; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
; FILE REFERENCE: 2676-466IUS
; CURRENT APPLICATION NUMBER: US/09/764, 803A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: PCT/EP99/04939
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EP 98202422.6
; PRIOR FILING DATE: 1999-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-764-803A-2

```

```

Query Match 75.4%; Score 934.5; DB 10; Length 257;
Best Local Similarity 70.9%; Pred. No. 2.8e-83;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

```

```

QY 1 MSNPRSLSEEEKYDMSGALALILCTVARESEEDLDALHMPROLRESTMKRDPPTAEQ 60
DB 5 MSDPQLQEEERYDMSGARLALILCTVARESEEDLDALHMPROLRESTMKRDPPTAEQ 64
QY 61 FOEELKFOQAIDSRDPVSCAFVVLMAHGREGLKGEDGEMVLENLFEALNNKNCAL 120
DB 65 FLEELDEFQQTIDWEEBVSQAFVVLMAHGREGLKGEDGEMVLENLFEALNNKNCAL 124
QY 121 RAKPKVYIIQACRGEQDPEGTGDEIWMYIKDSPOTIPYTDALHY 168
DB 125 RAKPKVYIIQACRGEQDPEGTGDEIWMYIKDSPOTIPYTDALHY 183
QY 169 YSTVEGIYARHDQKSCFIQTLVDVFTKRKGHILELLEVTNRMAEALVOEGKARKTN 228
DB 184 YSTVEGIYARHDQKSCFIQTLVDVFTKRKGHILELLEVTNRMAEALVOEGKARKTN 243
QY 229 PEIQTSLRKRLYLQ 242
DB 244 PEIQTSLRKRLYLQ 257

```

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RESULT 8
US-09-989-903-2
; Sequence 2, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

```

; TITLE OF INVENTION: AND METHODS OF USE  
 ; FILE REFERENCE: 480140.434D1  
 ; CURRENT APPLICATION NUMBER: US/09/989,903  
 ; CURRENT FILING DATE: 2002-04-11  
 ; NUMBER OF SEQ ID NOS: 78  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 260  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-989-903-2

Query Match 75.4%; Score 934.5; DB 10; Length 260;  
 Best Local Similarity 70.9%; Pred. No. 2.8e-83;  
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCTYKAREGSEEDLDALEHMFROLPFESTMKRDPDTAQ 60  
 DB 8 MSDPPLDEERYDMSGARLALILCTYKAREGSEEDLDALEHMFROLPFESTMKRDPDTAQ 67  
 QY 61 FOEELKFOQAIDSRDPVSCAFVLMAGRGSGFLKGEDEGEMVKNLELFEALNNKXQAL 120  
 DB 68 FLEELDEFQOTIDNNEBPVSCAFVLMAGRGSGFLKGEDEGEMVKNLELFEALNNKXQAL 127  
 QY 121 RAKPKVYIIQACRGEGRDPG-----ETVGDDEIWMVIXDSPTIPTYTDALHV 168  
 DB 128 RAKPKVYIIQACRGEGRDPGELRGNEELGDEDELGDE-VAVLKNPQSIPTYTDLHI 186  
 QY 169 YSTVGEYIAYRRDQKSCITQTLVDYFTKRGHILELLEVTYRRMAEALVQEGKARKTN 228  
 DB 187 YSTVGEYIAYRRDQKSGFIQTLVDYFTKRGHILELLEVTYRRMAEALVQEGKARKTN 246  
 QY 229 PEIQTSLRKRLYLQ 242  
 DB 247 PEVQSTLRKRLYLQ 260

RESULT 9  
 US-09-989-903-7  
 ; Sequence 7, Application US/09989903  
 ; Patent No. US20020146804A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
 ; TITLE OF INVENTION: AND METHODS OF USE  
 ; FILE REFERENCE: 480140.434D1  
 ; CURRENT APPLICATION NUMBER: US/09/989,903  
 ; CURRENT FILING DATE: 2002-04-11  
 ; NUMBER OF SEQ ID NOS: 78  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 230  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-09-989-903-7

Query Match 71.8%; Score 890; DB 10; Length 230;  
 Best Local Similarity 99.4%; Pred. No. 5.1e-79;  
 Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMSGALALILCTYKAREGSEEDLDALEHMFROLPFESTMKRDPDTAQ 60  
 DB 1 MSNPRLSEEEKYDMSGARLALILCTYKAREGSEEDLDALEHMFROLPFESTMKRDPDTAQ 60  
 QY 61 FOEELKFOQAIDSRDPVSCAFVLMAGRGSGFLKGEDEGEMVKNLELFEALNNKXQAL 120  
 DB 61 FOEELKFOQAIDSRDPVSCAFVLMAGRGSGFLKGEDEGEMVKNLELFEALNNKXQAL 120  
 QY 121 RAKPKVYIIQACRGEGRDPGELRGNEELGDEDELGDE-VAVLKNPQSIPTYTDALHV 174  
 DB 121 RAKPKVYIIQACRGEGRDPGELRGNEELGDEDELGDE-VAVLKNPQSIPTYTDALHV 174

RESULT 10  
 US-09-888-243-28  
 ; Sequence 28, Application US/09888243  
 ; Patent No. US20020136714A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horvitz, R. Robert  
 ; APPLICANT: Yuan, Junying  
 ; APPLICANT: Shih, Shai  
 ; TITLE OF INVENTION: Relatedness of Human Interleukin-1beta  
 ; TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory  
 ; FILE REFERENCE: 01997/211003  
 ; CURRENT APPLICATION NUMBER: US/09/888,243  
 ; CURRENT FILING DATE: 2001-06-22  
 ; PRIOR APPLICATION NUMBER: US 09/083,662  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: US 08/394,189  
 ; PRIOR FILING DATE: 1995-02-24  
 ; PRIOR APPLICATION NUMBER: US 08/282,211  
 ; PRIOR FILING DATE: 1994-07-11  
 ; PRIOR APPLICATION NUMBER: US 07/984,182  
 ; PRIOR FILING DATE: 1992-11-20  
 ; PRIOR APPLICATION NUMBER: US 07/897,788  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 451  
 ; TYPE: PRT  
 ; ORGANISM: Murine  
 US-09-888-243-28

Query Match 23.8%; Score 295; DB 10; Length 451;  
 Best Local Similarity 31.5%; Pred. No. 8e-21; Indels 36; Gaps 7;  
 Matches 75; Conservative 52; Mismatches 75;

QY 29 RGSEEDLDALEHMFROLPFESTMKRDPDTAQFOEELKFOQAIDSRDPVSCAFVLM 88  
 DB 218 RSGGVVDHTTLVTLFLKLGYNVHVLDOTAQOMQKLNFG-LPAHVTDSCV-VALLS 275  
 QY 89 HGRSEFLKGEDEGEMVKNLELFEALNNKXQALRAKPKVYIIQACRGEGRDPG----- 140  
 DB 276 HVEGEGIVGVDKTLQLOVEFRLFDNANCPSLONKPKMFIOACRGDETRGVDQDDGN 335  
 QY 141 -----ETVGDDEIWMVIXDSPTIPTYTDALHVGEVGEYIAYRRDQKSCFIQTLV 192  
 DB 336 HTQSPGCESDQKKEELMKR-----LPRSDMIGYACLGKNAAMRYTKRGSWYIEALT 390  
 QY 193 DVFTKR--KGHILELLEVTYRRMAEALVQEGKARKTN-----PEIQTSLRKRLYL 241  
 DB 391 QVFSERACDMHVADMLVKNALIKE-----REGYAETGERHCKEMSFYCSITLQGLYL 444

RESULT 11  
 US-09-989-903-63  
 ; Sequence 63, Application US/09989903  
 ; Patent No. US20020146804A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
 ; TITLE OF INVENTION: AND METHODS OF USE  
 ; FILE REFERENCE: 480140.434D1  
 ; CURRENT APPLICATION NUMBER: US/09/989,903  
 ; CURRENT FILING DATE: 2002-04-11  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 63  
 ; LENGTH: 74  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-989-903-63

Query Match 23.6%; Score 293; DB 10; Length 74;  
Best Local Similarity 77.8%; Pred. No. 1.1e-21;  
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 AREGSEEDLALHMFRLQRFESTMKRDPPTAEQFOEELKFOQAIDSREDPVSACAFVLM 87  
DB 1 ARESEVMEALERFRLKFEFTWKRDPTAQOQFLEIDFQOITIDNWEPEVSCAFVLM 60

QY 88 AHGREGFLKGED 99  
DB 61 AHGREGFLKGED 72

RESULT 12  
US-09-954-697-9  
Sequence 9, Application US/09954697  
Patent No. US2002010651A1  
GENERAL INFORMATION:  
APPLICANT: Alnemir, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES  
FILE REFERENCE: 480140.431D2  
CURRENT APPLICATION NUMBER: US/09/954.697  
CURRENT FILING DATE: 2001-09-14  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-954-697-9

Query Match 23.3%; Score 289; DB 10; Length 435;  
Best Local Similarity 31.1%; Pred. No. 2.9e-20;  
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLALHMFRLQRFESTMKRDPPTAEQFOEELKFOQAIDSREDPVSACAFVLM 88  
DB 202 RSGGVHDSTLVTLFKLGYDVHVLCDQTAQMOEKLQNFQ-LEAHVVTBSC-IVALLS 259

QY 89 HGRGEGFLKGEDEVKLENLEFALNNKNCQALRAKPKYVITIOACRGEPDPG----- 140  
DB 260 HGVEGAIVGVGKQLQLEVFOLFNNANCPSLQNKPKMFIOACRGDETRDGVDDQDGKN 319

QY 141 -----ETVGGDEIVWVINDSPOTIPPTYDALHVSVEEYIAYRRDQKSGSCITQLV 192  
DB 320 HAGSPGCESSDAGE-----KLPRKRLPTRSDMIGYACLKGTAAMRYTKRGSWYIEALA 374

QY 193 DVFTKR--KGHILELLEVTERRMAEALVOEGKARKTN-----PEIOSTLRKRLYL 241  
DB 375 QVFSERACDMHADMVLVKNALIKD----REGYAPGTEPHRCKENSEYCSITLRLHLYL 428

RESULT 13  
US-09-895-263-4  
Sequence 4, Application US/09895263  
Patent No. US20020076793A1  
GENERAL INFORMATION:  
APPLICANT: He, Wei-wu et al.  
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
Like Apoptosis Protease 3 and 4  
NUMBER OF SEQUENCE: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Ave.  
CITY: Rockville.  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/895.263  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PFI140  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-251-6015  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-895-263-4

Query Match 22.1%; Score 273.5; DB 10; Length 277;  
Best Local Similarity 31.9%; Pred. No. 5.1e-19;  
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

QY 9 EEKYMSGALALILCVTK-----AREGSEEDLALHMFRLQRFESTMKRDPPTA 58  
DB 34 DNSYKMDYPEWGLCIITINNKNFHKSTGWTSGTVDVANLRETFRNLYKVRNKGDLTR 93

QY 59 EQFOEELKFOQAIDSREDPVSACAFVLMAGREGFLKGEQG--EMVLEULEFALNNKN 116  
DB 94 EEIVELMDVSKEDSKSSSFVC---VLLSHGEGGIIFGTNGPVDLKKITNFF--RGDR 147

QY 117 COALRAKPKYVITIOACRGEPDPG-ETVGGDEIVWVINDSPOTIPPTYDALHVSVEGY 175  
DB 148 CRSLTGKRLFTIOACRGTEIDCGIETDSGVDDMAC---HKIPVEADFLYASTARGY 203

QY 176 IAYRHDDKSCFIOTLVDFTK--RKGHILELLEVTERRMA-EALVQ---EGKARKTNP 229  
DB 204 YSWRNSKDGSMFIOQLCMKQYADKLEFPHILTRVNRKVAETEFESFDFATFPAKKQIP 263

QY 230 EIOSTLRKRLYL 240  
DB 264 CIVSMLTRKELY 274

RESULT 14  
US-10-103-448-3  
Sequence 3, Application US/10103448  
Patent No. US2002015579A1  
GENERAL INFORMATION:  
APPLICANT: Krebs, Joseph F.  
APPLICANT: Stinivaasan, Anu  
APPLICANT: Filtz, Lawrence C.  
TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS  
TITLE OF INVENTION: COMPARING THE SAME AND METHODS OF USE THEREFOR  
FILE REFERENCE: 480140.468D1  
CURRENT APPLICATION NUMBER: US/10/103.448  
CURRENT FILING DATE: 2002-03-20  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 264  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-103-448-3

Query Match 22.0%; Score 272.5; DB 9; Length 264;  
Best Local Similarity 31.9%; Pred. No. 5.9e-19;  
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

Job time : 10.6414 secs

Qy 9 EEKYMSSGAALLILICVTK-----ARSGSEDLDALEHMFQRLFESTMKRDPTA 58  
Db 21 DNSYKMDYPEWGLCTIINNKNFHKSTGMTSRSGTDVDAANLRETFNRLKYEVANKNDLTR 80  
Qy 59 EFOFELEKFOQAISREDPVSCAFVILMAHGREGLKGEDG--EMVKLENLFEALNNKN 116  
Db 81 BEIVELMRDVSKEDHSKSSFC---VLSHGEGLIIFGTNGPVDLKITNFF--RGDR 134  
Qy 117 COALRAKPKVYIIQACRGEQRPDGE-ETVGGDEIWMYIKDSPOTIPTYDALHVSIVGEY 175  
Db 135 CRSLTGKPKLFIQACRGTELDGIEITDSGVDDMAC---HKIPVDADFLYAYSTAPGY 190  
Qy 176 IAYRHQKSGCFTQLVDVFTK--RKGHLLELTVTRMA--EAEIVQ--EGKARKTNP 229  
Db 191 YSWRNSKDSWFIQSICAMLKQYADKLEFPHMLITRVNRKVATEFESFSPDATFHAQQIP 250  
Qy 230 EIQSTLRKRLY 240  
Db 251 CIVSMILTKELY 261

## RESULT 15

US-10-108-929-3  
; Sequence 3, Application US/10108929  
; Publication No. US20020197702A1  
; GENERAL INFORMATION:  
; APPLICANT: Krebs, Joseph F.  
; APPLICANT: Srinivasan, Anu  
; APPLICANT: Fritz, Lawrence C.  
; APPLICANT: Mu, Joseph C.  
; TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3, COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING THE SAME AND METHODS OF USE THEREFOR  
; FILE REFERENCE: 480140.468D2  
; CURRENT APPLICATION NUMBER: US/10/108,929  
; CURRENT FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-108-929-3

Query Match 22.0%; Score 272.5; DB 9; Length 264;  
Best Local Similarity 31.9%; Pred. No. 5.9e-19;  
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

Qy 9 EEKYMSSGAALLILICVTK-----ARSGSEDLDALEHMFQRLFESTMKRDPTA 58  
Db 21 DNSYKMDYPEWGLCTIINNKNFHKSTGMTSRSGTDVDAANLRETFNRLKYEVANKNDLTR 80  
Qy 59 EFOFELEKFOQAISREDPVSCAFVILMAHGREGLKGEDG--EMVKLENLFEALNNKN 116  
Db 81 BEIVELMRDVSKEDHSKSSFC---VLSHGEGLIIFGTNGPVDLKITNFF--RGDR 134  
Qy 117 COALRAKPKVYIIQACRGEQRPDGE-ETVGGDEIWMYIKDSPOTIPTYDALHVSIVGEY 175  
Db 135 CRSLTGKPKLFIQACRGTELDGIEITDSGVDDMAC---HKIPVDADFLYAYSTAPGY 190  
Qy 176 IAYRHQKSGCFTQLVDVFTK--RKGHLLELTVTRMA--EAEIVQ--EGKARKTNP 229  
Db 191 YSWRNSKDSWFIQSICAMLKQYADKLEFPHMLITRVNRKVATEFESFSPDATFHAQQIP 250  
Qy 230 EIQSTLRKRLY 240  
Db 251 CIVSMILTKELY 261

Search completed: February 26, 2003, 12:28:00



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:17:56 ; Search time 13.0159 Seconds  
(without alignments)  
547.048 Million cell updates/sec

Title: US-09-989-903-5  
Perfect score: 1239  
Sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKTNPETOSTLRRLYLQ 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTDUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	242	4	US-09-187-789-5
2	1065	86.0	214	4	US-09-187-789-9
3	934.5	75.4	260	4	US-09-187-789-2
4	934.5	75.4	260	4	US-09-139-600-2
5	890	71.8	230	4	US-09-187-789-7
6	293	23.6	74	4	US-09-187-789-63
7	293	23.6	74	4	US-09-119-600-58
8	289	23.3	421	4	US-08-983-502-10
9	289	23.3	421	5	PCT-US96-10521-10
10	289	23.3	435	3	US-08-258-287B-53
11	289	23.3	435	3	US-08-368-704C-51
12	289	23.3	435	4	US-09-561-756-9
13	289	23.3	435	4	US-09-227-721-9
14	289	23.3	435	5	US-08-816-075-2
15	289	23.3	435	5	PCT-US94-07127A-4
16	289	23.3	441	3	US-08-258-287B-44
17	289	23.3	441	3	US-08-368-704C-43
18	278.5	22.5	277	2	US-08-890-542A-2
19	273.5	22.1	277	3	US-08-591-605-2
20	273.5	22.1	277	3	US-08-964-308-6
21	273.5	22.1	277	3	US-08-462-969B-4
22	273.5	22.1	277	3	US-08-964-313-6
23	273.5	22.1	277	4	US-09-069-138-6
24	272.5	22.0	277	4	US-09-561-756-12
25	272.5	22.0	277	4	US-09-227-721-12
26	272.5	22.0	277	4	US-08-983-502-30
27	272.5	22.0	277	5	PCT-US96-10521-30

28	263.5	21.3	277	3	US-08-964-308-10	Sequence 10, Appl
29	263.5	21.3	277	3	US-08-964-313-10	Sequence 10, Appl
30	263.5	21.3	277	3	US-09-069-138-10	Sequence 10, Appl
31	257	20.7	503	3	US-08-258-287B-36	Sequence 36, Appl
32	257	20.7	503	3	US-08-368-704C-36	Sequence 36, Appl
33	256	20.7	303	4	US-09-561-756-24	Sequence 24, Appl
34	256	20.7	303	4	US-09-227-721-24	Sequence 24, Appl
35	256	20.7	303	4	US-08-556-627A-2	Sequence 2, Appl
36	252	20.3	303	3	US-08-462-969B-2	Sequence 2, Appl
37	251	20.3	505	2	US-08-394-189B-5	Sequence 5, Appl
38	251	20.3	505	5	PCT-US93-05701-20	Sequence 20, Appl
39	251	20.3	505	5	PCT-US93-05705-5	Sequence 5, Appl
40	249	20.1	497	3	US-08-258-287B-37	Sequence 37, Appl
41	249	20.1	497	3	US-08-368-704C-37	Sequence 37, Appl
42	248	20.0	346	2	US-08-618-408B-2	Sequence 2, Appl
43	248	20.0	479	1	US-08-665-220-2	Sequence 2, Appl
44	248	20.0	479	4	US-09-291-692-2	Sequence 2, Appl
45	248	20.0	479	4	US-09-561-756-33	Sequence 33, Appl

## ALIGNMENTS

```

RESULT 1
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemeti, Emad S.
; APPLICANT: Fernandez-Alnemeti, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187, 789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-187-789-5

Query Match      100.0%; Score 1239; DB 4; Length 242;
Best Local Similarity 100.0%; Pred No. 2.4e-122;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFRLRFESTMKRDPTRAEQ 60
DQ      1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFRLRFESTMKRDPTRAEQ 60
QY      61 FOELEKFOQAIDREDPVSCAFVYLMAGREGFLKGEDGMVLEULFELNNKNCQAL 120
DQ      61 FOELEKFOQAIDREDPVSCAFVYLMAGREGFLKGEDGMVLEULFELNNKNCQAL 120
QY      121 RAKKVVYIIQACREQODPGETVSGDEIWMYIKDSPOTIPYTDALHYSTVEGIAYRH 180
DQ      121 RAKKVVYIIQACREQODPGETVSGDEIWMYIKDSPOTIPYTDALHYSTVEGIAYRH 180
QY      181 DQKSCFIQTLVDVFTKRKGHILLETVRMAEALVQEGKARKTNPETOSTLRRLRY 240
DQ      181 DQKSCFIQTLVDVFTKRKGHILLETVRMAEALVQEGKARKTNPETOSTLRRLRY 240
QY      241 LQ 242
DQ      241 LQ 242

RESULT 2
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:

```

APPLICANT: Alnemri, Emed S.  
APPLICANT: Fernandez-Alnemri, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHODS OF USE  
FILE REFERENCE: 480140.434C1  
CURRENT APPLICATION NUMBER: US/09/187,789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-187-789-9

Query Match 86.0%; Score 1065; DB 4; Length 214;  
Best Local Similarity 88.0%; Pred. No. 3.8e-104;  
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MSNPRLSEEEKYDMSGALALILCTVKAREGSEEDLDALHMFQRLRFESTMKRDPDPAQ 60  
DB 1 MSNPRLSEEEKYDMSGARLALILCTVKAREGSE----- 34  
QY 61 FOELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDEMYKLENI.FEALNNKNCQAL 120  
DB 35 --EELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDEMYKLENI.FEALNNKNCQAL 92  
QY 121 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPTQITPTTDLAHVSTVEGYIAYRH 180  
DB 93 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPTQITPTTDLAHVSTVEGYIAYRH 152  
QY 181 DQKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTNEIOSTLRKRLY 240  
DB 133 DQKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTNEIOSTLRKRLY 212  
QY 241 LQ 242  
DB 213 LQ 214

RESULT 3  
US-09-187-789-2  
Sequence 2, Application US/09187789  
Patent No. 6340740  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emed S.  
APPLICANT: Fernandez-Alnemri, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHODS OF USE  
FILE REFERENCE: 480140.434C1  
CURRENT APPLICATION NUMBER: US/09/187,789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-187-789-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;  
Best Local Similarity 70.9%; Pred. No. 2.6e-90;  
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCTVKAREGSEEDLDALHMFQRLRFESTMKRDPDPAQ 60  
DB 8 MSNPRLSEEEKYDMSGARLALILCTVKAREGSEEDLDALHMFQRLRFESTMKRDPDPAQ 67  
QY 61 FOELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDEMYKLENI.FEALNNKNCQAL 120  
DB 68 FLEELDEFQOTIDNMBEVPVSCAFVYLMAGREGFLKGEDEMYKLENI.FEALNNKNCQAL 127  
QY 121 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPTQITPTTDLAHV 168

DB 128 RGRKRVYIIQACRGHRDPGEELRGNEELGDEBELGDE--VAVLKNNPOSIPYTDLHI 186  
QY 169 YSTVEGYIAYRHDKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 228  
DB 187 YSTVEGYIAYRHDKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 246  
QY 229 PEIOSTLRKRLYLQ 242  
DB 247 PEIOSTLRKRLYLQ 260

RESULT 4  
US-09-139-600-2  
Sequence 2, Application US/09139600  
Patent No. 643628  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emed S.  
APPLICANT: Fernandez-Alnemri, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHOD OF USE  
FILE REFERENCE: 480140.434  
CURRENT APPLICATION NUMBER: US/09/139,600  
CURRENT FILING DATE: 1998-08-25  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-139-600-2

Query Match 75.4%; Score 934.5; DB 4; Length 260;  
Best Local Similarity 70.9%; Pred. No. 2.6e-90;  
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCTVKAREGSEEDLDALHMFQRLRFESTMKRDPDPAQ 60  
DB 8 MSNPRLSEEEKYDMSGARLALILCTVKAREGSEEDLDALHMFQRLRFESTMKRDPDPAQ 67  
QY 61 FOELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDEMYKLENI.FEALNNKNCQAL 120  
DB 68 FLEELDEFQOTIDNMBEVPVSCAFVYLMAGREGFLKGEDEMYKLENI.FEALNNKNCQAL 127  
QY 121 RAKPKVYIIQACRGORPGEIVGDEIWMVKDSPTQITPTTDLAHV 168  
DB 128 RAKPKVYIIQACRGHRDPGEELRGNEELGDEBELGDE--VAVLKNNPOSIPYTDLHI 186  
QY 169 YSTVEGYIAYRHDKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 228  
DB 187 YSTVEGYIAYRHDKSGCFIQTLDVFTKRGHILLETETVRMAEAEIVQEGKARKTN 246  
QY 229 PEIOSTLRKRLYLQ 242  
DB 247 PEIOSTLRKRLYLQ 260

RESULT 5  
US-09-187-789-7  
Sequence 7, Application US/09187789  
Patent No. 6340740  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emed S.  
APPLICANT: Fernandez-Alnemri, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
TITLE OF INVENTION: AND METHODS OF USE  
FILE REFERENCE: 480140.434C1  
CURRENT APPLICATION NUMBER: US/09/187,789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 230

TYPE: PRT  
ORGANISM: Homo sapien  
US-09-187-789-7

Query Match 71.8%; Score 890; DB 4; Length 230;  
Best Local Similarity 99.4%; Pred. No. 1e-85;  
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEKYDMSGALALILCTKAREGSEEDLALHEMFROLFEESTMKSDPTAEQ 60  
DB 1 MSNPSLEEKYDMSGALALILCTKAREGSEEDLALHEMFROLFEESTMKSDPTAEQ 60  
QY 61 FOEELKFOAIDSRDPSCAFYVLAHGREGLKGEDEMYLLENLFEALNNKCOAL 120  
DB 61 FOEELKFOAIDSRDPSCAFYVLAHGREGLKGEDEMYLLENLFEALNNKCOAL 120  
QY 121 RAKPKYIIQACRGQDPRGTGDEIVWIKSPQTIPTTALHVSIVEG 174  
DB 121 RAKPKYIIQACRGQDPRGTGDEIVWIKSPQTIPTTALHVSIVEG 174

## RESULT 6

US-09-187-789-63  
Sequence 63, Application US/09187789  
Patent No. 6340740  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emdad S.  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
FILE REFERENCE: 480140.434C1  
CURRENT APPLICATION NUMBER: US/09/187,789  
CURRENT FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 63  
LENGTH: 74  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-187-789-63

Query Match 23.6%; Score 293; DB 4; Length 74;  
Best Local Similarity 77.8%; Pred. No. 1.1e-23;  
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARSESEDLALHEMFROLFEESTMKSDPTAEQFOEELKFOAIDSRDPSCAFYVLM 87  
DB 1 ARSESEVDMELERMFRLKFEESTMKSDPTAEQFLBELDFQOTIDWEEBVSACAFVLM 60  
QY 88 AHGREGLKGED 99  
DB 61 AHGREGLKGED 72

## RESULT 7

US-09-139-600-58  
Sequence 58, Application US/09139600  
Patent No. 6432628  
GENERAL INFORMATION:  
APPLICANT: Fernandez-Alnemri, Teresa  
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING  
FILE REFERENCE: 460140.434  
CURRENT APPLICATION NUMBER: US/09/139,600  
CURRENT FILING DATE: 1998-08-25  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 58  
LENGTH: 74  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-139-600-58

Query Match 23.6%; Score 293; DB 4; Length 74;  
Best Local Similarity 77.8%; Pred. No. 1.1e-23;  
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARSESEDLALHEMFROLFEESTMKSDPTAEQFOEELKFOAIDSRDPSCAFYVLM 87  
DB 1 ARSESEVDMELERMFRLKFEESTMKSDPTAEQFLBELDFQOTIDWEEBVSACAFVLM 60  
QY 88 AHGREGLKGED 99  
DB 61 AHGREGLKGED 72

## RESULT 8

US-08-983-502-10  
Sequence 10, Application US/08983502  
Patent No. 639327  
GENERAL INFORMATION:  
APPLICANT: David WALLACH  
APPLICANT: Mark P. BOLDIN  
APPLICANT: Tanya M. GONCHAROV  
APPLICANT: Yuri V. GOLISEV  
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Broadway and Neimark  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,502  
FILING DATE: 16-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10521  
FILING DATE: 14-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114,615  
FILING DATE: 16-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114,986  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 115,319  
FILING DATE: 14-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 116,588  
FILING DATE: 27-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 117,932  
FILING DATE: 16-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Broadway, Roger L.  
REGISTRATION NUMBER: 25,618  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 421 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-983-502-10

Query Match 23.3%; Score 289; DB 4; Length 421;

Best Local Similarity 31.1%; Pred. No. 3.5e-22; Indels 36; Gaps 7;

Matches 74; Conservative 51; Mismatches 77;

QY 29 REGSEEDLDALHMFROQLFEFSTMKRDPPTAEQFOEELKFOQAIDSRDPVSCAFVYMA 88

DB 188 RSGGVNDHSTLVTLPKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDS-C-IVALLS 245

QY 89 HGREFLKGEDEGVKYLELFEALNNKQCALRAKPKYIIQACRGEQDPG----- 140

DB 246 HVEGAIVGVDPKLLQLOEVFQLPFNANCPSLQNKPKMFFIOACRGDETRDGVQDQDGN 305

QY 141 -----ETVGGDEIVMVIKDSPTPIPTYDALHVSVEGYIAYRHDKSGSCFIOTLV 192

DB 306 HAGSPGCESDGKE-----KLPPKRLPTRSDMTCGYACLGTAAMRNTRKGSWYTEALA 360

QY 193 DVFTKR--KGHLELLEVTTRMAEALVQEGKARKTN-----PEIOSTLRKRLYL 241

DB 361 QVFSRACDMHVDMLVKNALIKD----REGYAPGTEFHCKMSEYCSITLCHRLYL 414

RESULT 9

PCT-US96-10521-10

Sequence 10, Application PC/TUS9610521

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

NUMBER OF SEQUENCES: 34

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10521

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,615

FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 115,319

FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,986

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 116,588

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117,932

FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 421 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-10521-10

Query Match 23.3%; Score 289; DB 5; Length 421;

Best Local Similarity 31.1%; Pred. No. 3.5e-22; Indels 36; Gaps 7;

Matches 74; Conservative 51; Mismatches 77;

QY 29 REGSEEDLDALHMFROQLFEFSTMKRDPPTAEQFOEELKFOQAIDSRDPVSCAFVYMA 88

DB 188 RSGGVNDHSTLVTLPKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDS-C-IVALLS 245

QY 89 HGREFLKGEDEGVKYLELFEALNNKQCALRAKPKYIIQACRGEQDPG----- 140

DB 246 HVEGAIVGVDPKLLQLOEVFQLPFNANCPSLQNKPKMFFIOACRGDETRDGVQDQDGN 305

QY 141 -----ETVGGDEIVMVIKDSPTPIPTYDALHVSVEGYIAYRHDKSGSCFIOTLV 192

DB 306 HAGSPGCESDGKE-----KLPPKRLPTRSDMTCGYACLGTAAMRNTRKGSWYTEALA 360

QY 193 DVFTKR--KGHLELLEVTTRMAEALVQEGKARKTN-----PEIOSTLRKRLYL 241

DB 361 QVFSRACDMHVDMLVKNALIKD----REGYAPGTEFHCKMSEYCSITLCHRLYL 414

RESULT 10

US-08-258-287B-53

Sequence 53, Application US/08258287B

Parent No. 6083735

GENERAL INFORMATION:

APPLICANT: Yuan, Junyong

APPLICANT: Mura, Masayuki

TITLE OF INVENTION: Programmed Cell Death Genes and Proteins

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/258,287B

FILING DATE: 10-JUN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/080,850

FILING DATE: 24-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Lawrence B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609,3920001

TELEPHONE: (202) 371-2500

TELEFAX: (202) 371-2540

TELEX: 248636 SSX

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 435 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-258-287B-53

Query Match 23.3%; Score 289; DB 3; Length 435;

Best Local Similarity 31.1%; Pred. No. 3.6e-22; Indels 36; Gaps 7;

Matches 74; Conservative 51; Mismatches 77;

QY 29 REGSEEDLDALHMFROQLFEFSTMKRDPPTAEQFOEELKFOQAIDSRDPVSCAFVYMA 88

DB 202 RSGGVNDHSTLVTLPKLGVDVHVLCDQTAQEMQEKLNFAQ-LPAHRTVDS-C-IVALLS 259

QY 89 HGREFLKGEDEGVKYLELFEALNNKQCALRAKPKYIIQACRGEQDPG----- 140

DB 260 HVEGAIVGVDPKLLQLOEVFQLPFNANCPSLQNKPKMFFIOACRGDETRDGVQDQDGN 319

QY 141 -----ETVGGDEIVMVIKDSPTPIPTYDALHVSVEGYIAYRHDKSGSCFIOTLV 192

DB 320 HAGSPGCESDGKE-----KLPPKRLPTRSDMTCGYACLGTAAMRNTRKGSWYTEALA 374

QY 193 DVFTKR--KGHLELLEVTTRMAEALVQEGKARKTN-----PEIOSTLRKRLYL 241

Db 375 QVSEBRACDMHVADMLVKVNAALIKD---REGYAPGTEFFHRCCKEMSEYCSITLCHNLYL 428

## RESULT 11

US-08-368-704C-51  
Sequence 51, Application US/08368704C  
Patent No. 6087160  
GENERAL INFORMATION:  
APPLICANT: Yuan, Junying  
APPLICANT: Miura, Masayuki  
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/368,704C  
FILING DATE: 4-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/258,287  
FILING DATE: 10-JUN-1994  
CLASSIFICATION: 435  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/080,850  
FILING DATE: 24-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 0609,3920002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
TELEX: 248636 SSK  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 435 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-368-704C-51

Query Match 23.3%; Score 289; DB 3; Length 435;  
Best Local Similarity 31.1%; Pred. No. 3,6e-22;  
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLALHEMFROLPRESTKRDPTAEQFOEELKFOQAIDSREDPVSCAFVVLMA 88  
DB 202 RSGGDVHSTLVTLFKLGDVHVLCDOQAQOEKQNFQO-LPARHYVDS-C-IVALLS 259  
QY 89 HGREGLKGEDGEMVVKLENLFEALNNKQCALRAKPKVYIIQACRGEORDPG----- 140  
DB 260 HGVEGAIYGVADGKLLQOEVFQLPDNNANCPSLQNKPKMFFIOACRGDETRDGVDOOGKN 319  
QY 141 -----ETVGGDEIVMWIKDSQPTIPTYTDALHVTSTEGYIAYRHDDQKSCFIOTLV 192  
DB 320 HAGSPGCEESDAGE-----KLPRMRLPTRSDMTCGYACLGTAAMRTKRGSWYIEALA 374  
QY 193 DVFTKR--KGHILELLEVTFRMAEALVOEGKARKTN-----PEIOSTLRKRLYL 241  
DB 375 QVSEBRACDMHVADMLVKVNAALIKD---REGYAPGTEFFHRCCKEMSEYCSITLCHNLYL 428

RESULT 12  
US-09-561-756-9  
Sequence 9, Application US/09561756  
Patent No. 6376226  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
FILE REFERENCE: 480140,431  
CURRENT APPLICATION NUMBER: US/09/561,756  
CURRENT FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 09/227,721  
PRIOR FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-561-756-9

Query Match 23.3%; Score 289; DB 4; Length 435;  
Best Local Similarity 31.1%; Pred. No. 3,6e-22;  
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLALHEMFROLPRESTKRDPTAEQFOEELKFOQAIDSREDPVSCAFVVLMA 88  
DB 202 RSGGDVHSTLVTLFKLGDVHVLCDOQAQOEKQNFQO-LPARHYVDS-C-IVALLS 259  
QY 89 HGREGLKGEDGEMVVKLENLFEALNNKQCALRAKPKVYIIQACRGEORDPG----- 140  
DB 260 HGVEGAIYGVADGKLLQOEVFQLPDNNANCPSLQNKPKMFFIOACRGDETRDGVDOOGKN 319  
QY 141 -----ETVGGDEIVMWIKDSQPTIPTYTDALHVTSTEGYIAYRHDDQKSCFIOTLV 192  
DB 320 HAGSPGCEESDAGE-----KLPRMRLPTRSDMTCGYACLGTAAMRTKRGSWYIEALA 374  
QY 193 DVFTKR--KGHILELLEVTFRMAEALVOEGKARKTN-----PEIOSTLRKRLYL 241  
DB 375 QVSEBRACDMHVADMLVKVNAALIKD---REGYAPGTEFFHRCCKEMSEYCSITLCHNLYL 428

RESULT 13  
US-09-227-721-9  
Sequence 9, Application US/09227721  
Patent No. 6379950  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
FILE REFERENCE: 480140,431  
CURRENT APPLICATION NUMBER: US/09/227,721  
CURRENT FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 435  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-227-721-9

Query Match 23.3%; Score 289; DB 4; Length 435;  
Best Local Similarity 31.1%; Pred. No. 3,6e-22;  
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 141 -----ETVGDDEIWMVKDSPTIPTYTDAHVSTVEGYIAYRHDKGSCFIQTLV 192  
 Db 320 HAGSPGCESDAGKE-----KLPKMRLLPTRSDMIGVACLGKGTAMRNTKRGSWYTEALA 374  
 QY 193 DVFTKR--KGHLELLTEVTRMAEALVQSGKARKN-----PEIQSTLRKRLYL 241  
 Db 375 QVFSERACDMHVADMLVKVNALIKD---REGYAPGTEFHRCKEMSEYCSLTCRLHYL 428

RESULT 14  
 US-08-816-075-2  
 ; Sequence 2, Application US/08816075  
 ; Patent No. 6416753

GENERAL INFORMATION:  
 APPLICANT: Yuan, Junying  
 APPLICANT: Friedlander, Robert  
 TITLE OF INVENTION: Programmed Cell Death and Interleukin-1  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Ave., N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/816.075  
 FILING DATE: 13-MAR-1997  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/013,524  
 FILING DATE: 15-MAR-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bugalsky, Lawrence B.  
 REGISTRATION NUMBER: 35,086  
 REFERENCE/DOCKET NUMBER: 0609,421001/JAG/LBB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 435 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-816-075-2

Query Match 23.3%; Score 289; DB 4; Length 435;  
 Best Local Similarity 31.1%; Pred. No. 3,6e-22;  
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEDDALAHMFRQRLPESTMKRDPPTAQOFOEELKFOQALDSRDPVSCAFVULMA 88  
 Db 202 RSGGDVDSHTLVTLFKLGLGVHVLCDDTAQEMOEKQNFQO-LPAHRVTDSC-IVALLS 259  
 QY 89 HGREGLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG-----140  
 Db 260 HVEGAIYGVGDKLQLOEVFQLPFNANCPSLONKPKMFIQACRDEDTDRGVDDQDGKN 319  
 QY 141 -----ETVGDDEIWMVKDSPTIPTYTDAHVSTVEGYIAYRHDKGSCFIQTLV 192  
 Db 320 HAGSPGCESDAGKE-----KLPKMRLLPTRSDMIGVACLGKGTAMRNTKRGSWYTEALA 374  
 QY 193 DVFTKR--KGHLELLTEVTRMAEALVQSGKARKN-----PEIQSTLRKRLYL 241  
 Db 375 QVFSERACDMHVADMLVKVNALIKD---REGYAPGTEFHRCKEMSEYCSLTCRLHYL 428

RESULT 15  
 PCT-US94-07127A-4  
 ; Sequence 4, Application PC/TUS9407127A  
 ; GENERAL INFORMATION:  
 APPLICANT: HE, ET AL.  
 TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, and  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/07127A  
 FILING DATE: submitted herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FERRARO, GREGORY D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-184  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 435 AMINO ACIDS  
 TYPE: AMINO ACID  
 STRANDEDNESS:  
 TOPOLOGY: LINEAR 2  
 MOLECULE TYPE: PROTEIN  
 PCT-US94-07127A-4

Query Match 23.3%; Score 289; DB 5; Length 435;  
 Best Local Similarity 31.1%; Pred. No. 3,6e-22;  
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEDDALAHMFRQRLPESTMKRDPPTAQOFOEELKFOQALDSRDPVSCAFVULMA 88  
 Db 202 RSGGDVDSHTLVTLFKLGLGVHVLCDDTAQEMOEKQNFQO-LPAHRVTDSC-IVALLS 259  
 QY 89 HGREGLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG-----140  
 Db 260 HVEGAIYGVGDKLQLOEVFQLPFNANCPSLONKPKMFIQACRDEDTDRGVDDQDGKN 319  
 QY 141 -----ETVGDDEIWMVKDSPTIPTYTDAHVSTVEGYIAYRHDKGSCFIQTLV 192  
 Db 320 HAGSPGCESDAGKE-----KLPKMRLLPTRSDMIGVACLGKGTAMRNTKRGSWYTEALA 374  
 QY 193 DVFTKR--KGHLELLTEVTRMAEALVQSGKARKN-----PEIQSTLRKRLYL 241  
 Db 375 QVFSERACDMHVADMLVKVNALIKD---REGYAPGTEFHRCKEMSEYCSLTCRLHYL 428

Search completed: February 26, 2003, 12:22:04  
 Job time: 14.0159 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 26, 2003, 12:16:30 ; Search time 26.0319 Seconds  
(without alignments)  
1915.475 Million cell updates/sec

Title: US-09-989-903-5  
Perfect score: 1239  
Sequence: 1 MSNPSRLSEEEKYDMSCNALA.....KARKTNPETQSTLRKELYLQ 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_mhc.\*  
9: sp\_organelle.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293	23.6	452	11	O55194
2	289.5	23.4	423	13	O91B67
3	289	23.3	435	4	O9BUP7
4	284.5	23.0	283	13	O93417
5	274.5	22.2	277	6	O95ND5
6	274.5	22.2	383	13	O919L7
7	273.5	22.1	220	11	O9QWT4
8	273.5	22.1	277	4	O96ANI
9	272	22.0	399	13	O91B63
10	270.5	21.8	277	4	O96KP2
11	270	21.8	303	11	O88550
12	269.5	21.8	454	11	O9R0T0
13	269	21.7	482	13	O90WT1
14	266.5	21.5	282	13	O98UI8
15	260.5	21.0	403	13	O90WU0
16	257	20.7	476	13	O91B33

17	256	20.7	500	13	O91B64	O91B64 xenopus lae
18	256	20.7	520	13	O91B62	O91B62 xenopus lae
19	255	20.6	417	5	O9YIU6	O9YIU6 pristinichu
20	254.5	20.5	454	11	O9JHK1	O9JHK1 rattus norv
21	250.5	20.2	318	13	O91B65	O91B65 xenopus lae
22	248.5	20.1	496	4	O9COK4	O9COK4 homo sapien
23	248	20.0	479	4	O8WYQ8	O8WYQ8 homo sapien
24	246.5	19.9	538	4	O8TD15	O8TD15 homo sapien
25	242.5	19.6	276	11	O9D089	O9D089 mus musculu
26	241.5	19.5	276	11	O9SM47	O9SM47 mus musculu
27	239.5	19.3	416	4	O9B062	O9B062 homo sapien
28	235.5	19.0	182	6	O77623	O77623 ovib aries
29	235	19.0	277	11	O35397	O35397 rattus norv
30	233	18.8	480	11	O89110	O89110 m caspase 8
31	230.5	18.6	482	11	O9JHX4	O9JHX4 rattus norv
32	228.5	18.4	347	5	O9GV89	O9GV89 hydra atten
33	228.5	18.4	404	13	O9PDJ2	O9PDJ2 brachydantio
34	225	18.2	308	5	O9NHF9	O9NHF9 drosophila
35	225	18.2	308	5	O9VET9	O9VET9 drosophila
36	223.5	18.0	326	5	O9GV88	O9GV88 hydra atten
37	222	17.9	293	4	O9BOE7	O9BOE7 homo sapien
38	220.5	17.8	304	13	O93415	O93415 gallus gall
39	220	17.8	283	13	O42284	O42284 gallus gall
40	219.5	17.7	402	11	O91W32	O91W32 rattus norv
41	217.5	17.6	303	13	O91B66	O91B66 xenopus lae
42	211.5	17.1	393	11	O9R0S9	O9R0S9 mus musculu
43	211	17.0	373	11	O91XW7	O91XW7 rattus norv
44	210.5	17.0	302	13	O91B59	O91B59 oncorhynch
45	210.5	17.0	826	5	O9Y055	O9Y055 caenorhabdi

## ALIGNMENTS

RESULT 1  
ID O55194 PRELIMINARY; PRT; 452 AA.  
AC O55194;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE NEBD2/ICH-1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
CX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98087427; PubMed=9427555;  
RA Sato N., Milligen C.E., Uchiyama Y., Oppenheim R.W.;  
RT "Cloning and expression of the cDNA encoding rat caspase-2.";  
RL Gene 202:127-132(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;  
RA Jin K.L., Simon R.P., Graham S.H.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U77933; AAB95379.1; -;  
DR EMBL; AF136231; AAD33684.1; -;  
DR HSSP; P29466; 1ICE.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR002398; ICE.  
DR InterPro; IPR002318; ICE.  
DR InterPro; IPR001309; ICE\_P20.  
DR InterPro; IPR001309; CARD; 1.  
DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF00655; ICE\_P10; 1.  
DR Pfam; PF00656; ICE\_P20; 1.  
DR PRINTS; PR00376; IL1BCENZYM.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00115; CARD; 1.  
DR PROSITE; PS50209; CARD; 1.  
DR PROSITE; PS01122; CASPASE\_CYS; 1.  
DR PROSITE; PS01121; CASPASE\_HIS; 1.

DR PROSITE, PS50207, CASPASE\_P10; 1.  
 DR PROSITE, PS50208, CASPASE\_P20; 1.  
 SQ SEQUENCE 452 AA; 50728 MW; 03F9D096B8741CE3 CRC64;

Query Match 23.6%; Score 293; DB 11; Length 452;  
 Best Local Similarity 31.5%; Pred. No. 1,4e-16;  
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY REGSEEDLDALHEMFROLPFESTMKRDPTAEQFOEELKFOQAIDSRDPVSCAFVUMA 88  
 DB RSGGVDDHTLTATLTKLGYNVHLYDQTAQEMOKLQNFQA-LPAHRTDSC-IVALIS 276  
 QY 89 HGREGFLKGEDEGMVLENTLFEALNNKCOALRAKPKVYIIQACRGEQDPG----- 140  
 DB HVEGEGIVGVDKLLQLOEVFRLFDNANCPSLQNKPKMFFIOACRGDETRGVDDQDGN 336  
 QY 141 -----ETVGGDEIVWYIKDSPQTIPTYTDALHYSTVEGYIAYRHQKSCFIQTLV 192  
 DB 337 HAQSPGCESSDAGKSELMMR-----LPTPSDMIICGYACLKGNAMRNKRGSWYIEALT 391  
 QY 193 DVFTKR--KGHILELLEVTYRMAEALVOEGKARKTN-----PEIOSTLRKRLYL 241  
 DB 332 QVFSERACDMHVDMLVKVNALIKE-----REGYAPGTETFRCKEMSEYCSITLCQRLYL 445

## RESULT 2

Q91B67 PRELIMINARY; PRT; 423 AA.  
 ID Q91B67  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Caspase-2.  
 GN XCAPASE-2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20209426; PubMed=10744739;  
 RA Nakajima K., Takahashi A., Yaoita Y.,  
 RT "Structure, expression and function of the Xenopus laevis caspase  
 RT family";  
 RL J. Biol. Chem. 275:10484-10491(2000).  
 DR EMBL; AB038168; BAA94746.1; -.  
 DR HSSP; P29466; 1ICE.  
 DR MEROPS; C14.006; -.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; ILIBENZYM.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 423 AA; 47123 MW; E91EB1FD133F01FD CRC64;

Query Match 23.4%; Score 289.5; DB 13; Length 423;  
 Best Local Similarity 30.5%; Pred. No. 2.6e-16;  
 Matches 74; Conservative 51; Mismatches 71; Indels 47; Gaps 7;

QY 29 REGSEEDLDALHEMFROLPFESTMKRDPTAEQFOEELKFOQAIDSRDPVSCAF 83  
 DB 187 RCGGEVDLSTLEKLFSSLGVDVNCNLNAGSMWSQLAGFASLPVSHALDS-----CV 239

QY 84 VLMAGREGFLKGEDEGMVLENTLFEALNNKCOALRAKPKVYIIQACRGEQDPG--- 140  
 DB VAILSHGLDGAIVYGTGDKLVQLOEVFTALDNHACPOLQNKPKMFFIOACRGEETDRVDQ 299  
 QY 141 -----ETVGGDEIVWYIKDSPQTIPTYTDALHYSTVEGYIAYRHQKSCF 187  
 DB 300 RDGREGSPGCEQSDARERIKV-----RLPTQSDMICYACLKGVSLRNKRGSMF 353  
 QY 188 IQLVDVFTK--RKGHILELLEVTYRMAEALVOEGKARKTN-----PEIOSTLRK 238  
 DB 354 VQDLVSVFSQSHKQTHVADMLVKVNALIKE-----REGYAPGTETFRCKEMSEYCSITLCRD 409  
 QY 239 LYL 241  
 DB 410 LYL 412

## RESULT 3

Q9BUP7 PRELIMINARY; PRT; 435 AA.  
 ID Q9BUP7  
 AC Q9BUP7  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Similar to caspase 2.  
 DE Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SKIN;  
 RA Straubeberg R.;  
 RL Submitted (FEF-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002427; AA02427.1; -.  
 DR HSSP; P29466; 1ICE.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; ILIBENZYM.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 435 AA; 48869 MW; 10CFASALF9369E57 CRC64;

Query Match 23.3%; Score 289; DB 4; Length 435;  
 Best Local Similarity 31.1%; Pred. No. 2.9e-16;  
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLDALHEMFROLPFESTMKRDPTAEQFOEELKFOQAIDSRDPVSCAFVUMA 88  
 DB 202 RSGGVDDHTLTATLTKLGYDVHLYDQTAQEMOKLQNFQA-LPAHRTDSC-IVALIS 259  
 QY 89 HGREGFLKGEDEGMVLENTLFEALNNKCOALRAKPKVYIIQACRGEQDPG----- 140  
 DB HVEGEGIVGVDKLLQLOEVFRLFDNANCPSLQNKPKMFFIOACRGDETRGVDDQDGN 319  
 QY 141 -----ETVGGDEIVWYIKDSPQTIPTYTDALHYSTVEGYIAYRHQKSCFIQTLV 192  
 DB 320 HAQSPGCESSDAGKE-----KLPKRLPTPSDMIICGYACLKGTAMRNKRGSWYIEALA 374  
 QY 193 DVFTKR--KGHILELLEVTYRMAEALVOEGKARKTN-----PEIOSTLRKRLYL 241  
 DB 375 QVFSERACDMHVDMLVKVNALIKD-----REGYAPGTETFRCKEMSEYCSITLCRHLYL 428



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RESULT 4
093417 PRELIMINARY; PRT; 283 AA.
AC 093417;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149872; PubMed=10684799;
RA Johnson A.L., Bridgham J.T.;
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells.";
RL Biol. Reprod. 62:589-598(2000).
DR EMBL; AF083029; AAC32602.1; -.
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10.1.
DR Pfam; PF00656; ICE_p20.1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 23.0%; Score 284.5; DB 13; Length 283;
Best Local Similarity 30.3%; Pred. No. 4.2e-16;
Matches 76; Conservative 47; Mismatches 101; Indels 27; Gaps 7;

QY 7 LEEERYDMGSAALALILCVT-----KAREGSEEDLALHEMFRLQRFESTMKRP 56
DB 40 LPDSSYRNDYDEIGCVIINKNFHRTGLSSRGTDAASVREVFMKLGKVLNLDL 99
QY 57 TAEPQOELEKFOQAIDSREDPVSCAFVYLMAGREGFLKGEDEGMVLENLFEALNNK 116
DB 100 SSRDIFKLKLVSEEDHSHKSSPVC---VLISHGDEGLFYGTGDPFL-ELKVLTSLFRGDK 155
QY 117 CQALRAKPKVYIIACRGEGRPDGP--ETVGGDEIVMVIKDSPTPIPTVDLHVSTVEG 174
DB 156 CRSLAGKPKLFFIOACRTELDGSEADSGPDETVC-----QKTPVADPLVYASTAPG 209
QY 175 YIAVRHDKGSCFIOQLVDVFTK--RKGHILELLEVTNRMAEALV---QEGKARKTNP 229
DB 210 YYSWRNMAEGSWFIQSLCRLMKLKHARKLQILTRVNRVAVEYSSCTRODPNAKKQIP 269
QY 230 EIQSTLRKRLY 240
DB 270 CIVSMLTRKFLY 280

RESULT 5
0935ND5 PRELIMINARY; PRT; 277 AA.
AC 0935ND5;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334413; PubMed=11440638;
RA Muneta Y., Shimajima Y., Mori Y.;
RT "Porcine caspase-3: cloning and its activity during apoptosis of
RT porcine PK15 cells induced by porcine Fas-ligand.";
RL J. Interferon Cytokine Res. 21:409-415(2001).
DR EMBL; AB029345; BAB55544.1; -.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10.1.
DR Pfam; PF00656; ICE_p20.1.
DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 22.2%; Score 274.5; DB 6; Length 277;
Best Local Similarity 37.3%; Pred. No. 2.8e-15;
Matches 82; Conservative 27; Mismatches 94; Indels 17; Gaps 8;

QY 29 REGSEEDLALHEMFRLQRFESTMKRPDPTAEQFOELEKFOQAIDSREDPVSCAFVYLM 88
DB 64 RSGTDVDAANLREFTNLTKEVRNKNDLTREIELMHSHSKEDHSKRSSPFC---VLIS 120
QY 89 HGREGLKGEDEGMVLENLFEALNNKQCALRAKPKVYIIACRGEGRPDGP-ETVGGDE 147
DB 121 HGEGRKIFGTNGP-VDLKKLTSFFRGDCRRTLTGKPKLFIIOACRGTELDGIEITDGTGTE 179
QY 148 IVMYIKDSPTPIPTVDLHVSTVEGVYAVRHDKGSCFIOQLVDVFTKRGHILEL-- 205
DB 180 DDMAC---QKTPVADPLVYASTAPGYSWRNMAEGSWFIQSLCAAL-KQYVAKLELMH 234
QY 206 -LLEVTNRMA-EAELVQEGK---ARKTNPEIQSTLRKRLY 240
DB 235 ILTRVNRKVAVEPESFSTDSFPAKKQIPCLVSMLTRKFLY 274

RESULT 6
0919L7 PRELIMINARY; PRT; 383 AA.
AC 0919L7;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Caspase.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF333434; AAF66364.1; -.
DR HSSP; P29466; IICE.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR004020; PAAD_DAPIN_dom.
DR Pfam; PF00655; ICE_p10.1.
DR Pfam; PF00656; ICE_p20.1.
DR Pfam; PF02758; PAAD_DAPIN; 1.
DR PRINTS; PR00376; ILIBCNZYME.

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DR SMART, SM00115; CASC: 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 SO SEQUENCE 383 AA; 43966 MW; 21890871309774C3 CRC64;

Query Match 22.2%; Score 274.5; DB 13; Length 383;  
 Best Local Similarity 30.0%; Pred. No. 4.2e-15;  
 Matches 69; Conservative 49; Mismatches 83; Indels 29; Gaps 6;

QY 29 REGSEEDLALHMRQLAFESTMKRDPFAEQFQELKFOQALDSREPVSCAFVLM 88  
 DB 162 RGSSEKDEENMEKLKELDYQVAKRPNLSAKEMDEAIRFQREBKYS--DSAFVIVMS 219  
 QY 89 HGREGFLKG-----EDGEWVKLENLFEALNNKNCQALRAKPKVYIIQACRGEOR---- 137  
 DB 220 HKKRALMGVHYHRTNPSPDSFPVDVYRRLNSENCPALRDKPKVILLIACRGEGRVW 279  
 QY 138 ---DPGETVGDEIVMVIKDSPTQIPIYTDALHYSTVEGIAYRHDKSGCFIQTIVLD 193  
 DB 280 ASDGPDEIEIEDDDFVHKEK-----DFISLMSCTPDTKSYHVGNGTFYQTVLVD 331  
 QY 194 VFTK--RKCHILELLEVTERRMAEALVOEGKARKTNPEIQTSLRKRLYL 241  
 DB 332 VFICKAHEDHIEELFRKVLRRFHPMMI--GNFKQWACKDRATLPFLFYL 379

## RESULT 7

Q9QW14 PRELIMINARY; PRT; 220 AA.  
 ID Q9QW14  
 AC Q9QW14  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE CP932 apoptotic protease (Fragment).  
 GN CASP3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,  
 RA Fortin J.-P., Sekaly R.-P.;  
 RT "Multiple Pathways of Apoptosis Converging on the CPP32 Protease."  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U63720; AAD09504.1; -.  
 DR HSSP; P42574; IPAU.  
 DR MEROPS; C14.003; -.  
 DR MGD; MGI:107739; Casp3.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; ILIACENZYME.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Protease.  
 FT NON TER  
 SQ SEQUENCE 220 AA; 25050 MW; FE7F4857C4EBA544 CRC64;

Query Match 22.1%; Score 273.5; DB 11; Length 220;  
 Best Local Similarity 34.1%; Pred. No. 2.6e-15;  
 Matches 75; Conservative 34; Mismatches 96; Indels 15; Gaps 6;

QY 28 AREGSEEDLDALEHMRQLAFESTMKRDPFAEQFQELKFOQALDSREDPVSCAFVLM 87  
 DB 6 ANGTIDVDANLRFTFMGLKYQVRNKNDLTREDDILELMSVSKEDHSKSSPVC--VIL 62

QY 88 AHGREGFLKGDEWVKLENLFEALNNKNCQALRAKPKVYIIQACRGEORPG-ETVGD 146  
 DB 63 SHGDGVLYGTNGP-VELKKLTLSPFRGDYCSRLTCKPLFIQACRGTELDGIEIDSGT 121  
 QY 147 EIVMVIKDSPTQIPIYTDALHYSTVEGIAYRHDKSGCFIQTIVLDT--KRGHILE 204  
 DB 122 DEEMAC---OKIPYEAFLVASTAPGYYSWRNSKDSGFWIQLCSMLKYAHKIQFMH 177  
 QY 205 LITEVTRMA---EALVOEGKARKTNPEIQTSLRKRLYL 240  
 DB 178 ILTRVNRKVAIFESFSLDSTFHAKKQPCIVSMILTKELY 217

## RESULT 8

Q96AN1 PRELIMINARY; PRT; 277 AA.  
 ID Q96AN1  
 AC Q96AN1  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical 31.6 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC016926; AAH16926.1; -.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; ILIACENZYME.  
 DR PROSITE; PS01122; CASPASE\_CYS; UNKNOWN 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 277 AA; 31608 MW; 2F35CD3BCF7FE64A CRC64;

Query Match 22.1%; Score 273.5; DB 4; Length 277;  
 Best Local Similarity 31.9%; Pred. No. 3.4e-15;  
 Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

QY 9 EEKYDMGSAALALILCVTK-----AREGSEEDLDALEHMRQLAFESTMKRDPFA 58  
 DB 34 DNSYMGDYPENMLCIIINNKNPHKSTGMTSRGCTVDANLRFTFRNLKYVRNKNNDLTR 93  
 QY 59 EGFQSELEKFOQALDSREDPVSCAFVIMAHGRBGLKGEDEG--EMVYLENLFEALNNKN 116  
 DB 94 EEIVELMRDVSKEDEHSKSSPVC--VILSHGEEGIIIFGTNGPVLKKTITNFF--RQDR 147  
 QY 117 COALRAKPKVYIIQACRGEORPG-ETVGDSEIVMVIKDSPTQIPIYTDALHYSTVEGY 175  
 DB 148 CSSLGKPKPLFIQACRGTELDGIEIDSGVDDDAC---HKLIVEDFLYANSTADGY 203  
 QY 176 IAYRHDKSGCFIQTIVLVFTK--RKCHILELLEVTERRMA-EALVVO---EGKARKTNP 229  
 DB 204 YSMRNSKDSGFWIQLCSMLKNQYADKLEFMHILTRVNRKVAIFESFSDATFHAKKQIP 263  
 QY 230 EIQSTLRKRLYL 240  
 DB 264 CIVSMILTKELY 274

RESULT 9  
 Q9IB63 PRELIMINARY; PRT; 399 AA.  
 ID Q9IB63

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AC 091B61;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Caspase-9.
GN XcasPase-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
OX
RN
RP SEQUENCE FROM N.A.
RA MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yaota Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family".
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1QDU.
DR MEROPS; C14.010; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002398; Deact.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match 22.0%; Score 272; DB 13; Length 399;
Best Local Similarity 27.9%; Pred. No. 7.1e-15;
Matches 80; Conservative 40; Mismatches 107; Indels 60; Gaps 8;

QY 2 SNPRSLSEERK-YDMSGALALILCVT-----KAREGSEEDLALHEMPROLRPFES 50
DB 125 SRKGTLDKXDYPMSSPRIGECILINNMNPHCTGLSTRGSDIDRDKLANRMSFFFEV 184
QY 51 TMRKDPTEAEPFOEELKFFQALDSREDPVSCAFVYLMAGRE-----GFLKGEDEMV 103
DB 185 TVKXNLTGQAMHDLQALADQDHSLOD---CCLVVLISHGCEETHIQPGGVGTGDIRI 241
QY 104 KLENLFEALNNKNOALRAKPKVYIIQACRGEDRPBETVG----- 145
DB 242 PVEKIVSYFNGSKRPSLRGPKFIIFQACGDDQKCEVSETPPLSPSTSLQSDATP 301
QY 146 -----DEIVMWIKSPQTIPTPTALHVSFVEGYIARHDQKSCFIQTLVDVFTK 197
DB 302 VFSGEGRDV-----DAVSNIPFSDILVSYSTFFPGVSRDNGHSTSMYEVLDVSLAE 356
QY 198 RKG-HILELLTEVTRMAEELVQESKARKTNPETSLRKLRLYQ 242
DB 357 HAADLDQSLVNV-----ADGVSSKGTYKQIPGVFNFLKRFYFK 397

RESULT 10
Q96KP2 PRELIMINARY; PRT; 277 AA.
AC Q96KP2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Caspase-3.

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GN CASP3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
OX
RN
RP SEQUENCE FROM N.A.
RA Vallente F.M.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Oliver L.J.;
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit.".
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A413269; CAC080866.1; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31642 MW; 6162767B0D2DE021 CRC64;

Query Match 21.8%; Score 270.5; DB 4; Length 277;
Best Local Similarity 34.7%; Pred. No. 6.1e-15;
Matches 77; Conservative 35; Mismatches 91; Indels 19; Gaps 8;

QY 28 ARGSEEDLALHEMPROLRPFESTMKRDPTEAEPFOEELKFFQALDSREDPVSCAFVLM 87
DB 63 SRGTVDANLNETRNKLYEVNRKNDLTREIVELMRVSEKDSKSSPVC---VLL 119
QY 88 AHGREGLKGEDEG--EMVKLENLFEALNNKQALRAKPKVYIIQACRGEDRPB-ETVG 144
DB 120 SHBEGEIIFFCTGNPVDLKITTF--RGDRGRSLRGKPKPLFIQACRGTELDGIEFDS 176
QY 145 GDEIVMWIKSPQTIPTPTALHVSFVEGYIARHDQKSCFIQTLVDVFTK--RKGI 202
DB 177 GVDDDMAC---HKIPDADFVLAYSTAPGYSMRNSKDSWFIQSLCAMLKQYADLIER 232
QY 203 LEDTEVTRMA-EAEVLQ---EGKARKTNPETSLRKLRLY 240
DB 233 WHILTRVNRKVAEFPESFSDATFPAKQIPLCIIVSLTKELY 274

RESULT 11
O88550 PRELIMINARY; PRT; 303 AA.
AC O88550;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Caspase-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
OX
RN
RP SEQUENCE FROM N.A.
RA Tissue-Spleen;
RC Tissue-Spleen;
RA Forghani F., Roy S.;
RT "Rat caspase-7 sequence.".
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072124; AAC24011.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.

```

DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR PRINTS: PR00376; ILIBCNZYME.  
 DR SMART: SMO0115; CASC; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_p10; 1.  
 DR PROSITE: PS50208; CASPASE\_p20; 1.  
 DR SEQUENCE 303 AA; 34324 MW; A11728754BF199DD CRC64;

Query Match 21.8%; Score 270; DB 11; Length 303;  
 Best Local Similarity 32.6%; Pred. No. 7.5e-15;  
 Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;

QY 29 REGSEEDLDALHMFROLRFESTMKRDPFAEQFOELEKFOQAIDSRDPVSCAFVLA 88  
 DB 87 RRGDCKDAELFKFCRSIGFEVTAVNDCSCAMQDLRRASEDHNS--ACFACVLIS 143  
 QY 89 HGREGFLGDEGEMVLENIFFALNNKNCQALRAKPKVYIIQACRGEORDPGETVGDEI 148  
 DB 144 HGEENLITGKDC-VTPIDLTNHFGRDKTLLEKFLFIQACGTETLDDIOQDSGFI 202  
 QY 149 VMVIKDSQTIPTTYTDALHVSSTVEGYIAYRHQKSGCFIQTLDVFTK--RKHILELL 206  
 DB 203 NDTANPKYKIPVEADFLFAYSTVPGYYSWRNPGKSGMFWQALCSILNHEGKLEIMQIL 262  
 QY 207 TEVTRMAEALVOEGKAR---KTNPEIQSTLRKRLY 240  
 DB 263 TRVNDVARHFSQSDDPFRFNKKOIPCMVSMLTLYELY 300

## RESULT 12

Q9ROT0 PRELIMINARY; PRT; 454 AA.  
 AC Q9ROT0;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Caspase9.  
 GN CASP9.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20001956; Pubmed=10529400;  
 RA Fujita E., Jimbo A., Matuzaki H., Konishi H., Kikawa U., Momoi T.;  
 RT "Akt phosphorylation site found in human caspase-9 is absent in mouse  
 caspase-9";  
 RL Biochem. Biophys. Res. Commun. 264:550-555(1999).  
 DR EMBL; AB019600; BAA86895.1; -.  
 DR HSSP; P42574; IPAU.  
 DR MEROPS; C14.010; -.  
 DR MGD; MGI:127950; Casp9.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_p10.  
 DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; ILIBCNZYME.  
 DR SMART; SMO0114; CARD; 1.  
 DR SMART; SMO0115; CASC; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_p10; 1.  
 DR PROSITE; PS50208; CASPASE\_p20; 1.  
 DR SEQUENCE 454 AA; 50051 MW; 4614989AF623850F CRC64;

Query Match 21.8%; Score 269.5; DB 11; Length 454;

Best Local Similarity 30.6%; Pred. No. 1.4e-14;  
 Matches 76; Conservative 37; Mismatches 88; Indels 47; Gaps 7;

QY 29 REGSEEDLDALHMFROLRFESTMKRDPFAEQ---FOELEKFOQAIDSRDPVSCAFV 84  
 DB 218 RTGNNLRDKLHFRFRWRFEVYKNDLTAKQVYALMAMAHNRHLD-----CFVV 270  
 QY 85 VLMAGRE-----GFLKGDEGEMVLENIFFALNNKNCQALRAKPKVYIIQACRGEOR 137  
 DB 271 VILSHGQASHLQFPFAVYGTGDCSVSIEKLVNFNSGSGCFSLGKRPFIQACGGEOK 330  
 QY 138 D-----PGETVGDEIWMVIK-----DSPQITTYTDALHVSSTVEGYI 176  
 DB 331 DHGEVACTSSQGRITLDSSEPDAPVYQEGFRPLDLDVAVSLPTPSDILVYSTPFGFV 390  
 QY 177 AYRHQKSGCFIQTLDVFTK--RKHILELLTEVTRMAEALVOEGKARKTNPEIOST 234  
 DB 391 SWRDKKSGSWYETITLDGILEQWARSDDLRLRV-----ANAVSEKGYTKQIPGCENF 444  
 QY 235 LRKRLYIQ 242  
 DB 445 LRKRLFFK 452

## RESULT 13

Q9OWU1 PRELIMINARY; PRT; 482 AA.  
 AC Q9OWU1;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Caspase 8.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barton S., Bridgman J.T., Johnson A.L.;  
 RT "Caspase-8 and -9 expression in the hen ovary";  
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY057939; AAL23700.1; -.  
 DR InterPro; IPR001875; DED.  
 DR InterPro; IPR002138; ICE\_p10.  
 DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF01335; DED; 2.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00656; ICE\_p20; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; UNKNOWN\_1.  
 DR PROSITE; PS01121; CASPASE\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS50207; CASPASE\_p10; 1.  
 DR PROSITE; PS50208; CASPASE\_p20; 1.  
 DR PROSITE; PS50168; DED; 2.  
 DR SEQUENCE 482 AA; 54645 MW; 8E3936BE090BEF CRC64;

Query Match 21.7%; Score 269; DB 13; Length 482;  
 Best Local Similarity 29.7%; Pred. No. 1.6e-14;  
 Matches 66; Conservative 50; Mismatches 92; Indels 14; Gaps 5;

QY 27 KARESEEDLDALHMFROLRFESTMKRDPFAEQFOELEKFOQAIDSRDPVSCAFVLA 86  
 DB 261 KRRNGTHVDADLRLKRVFSNLHTVAEYDCDTELRNIVNNRCHDHNKD---CFVCCI 317  
 QY 87 MAHGREGFLKGDEGEMVLENIFFALNNKNCQALRAKPKVYIIQACRGEORDPG---ETV 143  
 DB 318 LSHGKDDIYGVDCGEVPIQELTTSFTGQNCOSLAKKRVFVQACQGDAYQKGVYIETD 377  
 QY 144 GDEIWMVTKSP---QITPTTYTDALHVSSTVEGYIAYRHQKSGCFIQTLDVFTK 197  
 DB 378 GSEQVYSLETDAFQDLDCIPSEADFLGNTTLDQDVSVSPSQGTWYIOSLCQHLESSCP 437  
 QY 198 RKGHILELLTEVTRMAEALVOEGKARKTNPEIOSTLRKRL 239

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Db 438 RGEDILTLITLTAQNOVSSK--IDKONAGKQMPSPSFTLRKTL 477
RESULT 14
Q98UI8 PRELIMINARY; PRT; 282 AA.
AC Q98UI8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Caspase-3.
GN CASP3.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN
RP SEQUENCE FROM N.A.
RA Yabu T., Okazaki T., Yamashita M.;
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
RT Mammalian Caspase-3."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047003; BAB32409.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR ZFIN; ZDB-GENE-011210-1; casp3.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM0115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E0932E CRC64;

Query Match 21.5%; Score 266.5; DB 13; Length 282;
Best Local Similarity 34.4%; Pred. No. 1.4e-14;
Matches 76; Conservative 38; Mismatches 90; Indels 17; Gaps 8;

Qy 29 REGSEBDLALHMFRLRFEESTYKRPDTAEQFOEELKFOQALDSRDPVSCAFV--VL 86
Db 67 RRGTDVAGNVMNVFRKLYIVKYNDQTVAOIMQVLTIV-----AHDHSCRCSLVCVL 121
Qy 87 MAHREGFLKGEDEMYKLENUFEALNNKNCOLRAKPKVYIIQACRGEORDPG-ETVGG 145
Db 122 LSHQDEGVFFFTD-TSVDLKSLLTSFRGDRCPSLVGKPKLFFIQACRSTELDPGVETDHT 180
Qy 146 DEIVMVIKDSPTIPTYDALHVSSTVEGYIAYRHQKSCFIQTLVDVFTK--RKGHIL 203
Db 181 DH--PDIPDGRERIPVADPLVAVSTVPGYVSWRNTMTGSMFIOGLCEMTKXGSELEL 238
Qy 204 ELTEVTRRM---EALVQEG-KARKTNPEIQSTLRKRLY 240
Db 239 QIMTRVNHKVALDPESITSNMPPGFAKQIPCIIVSWLTKEY 279

RESULT 15
Q90WUO PRELIMINARY; PRT; 403 AA.
AC Q90WUO;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Caspase 9 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton S., Bridgham J.T., Johnson A.L.;
RT "Caspase-8 and -9 expression in the hen ovary."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057940; AAL23701.1; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; ICE_p10; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS00235; MITOCH_CARRIER; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 403 AA; 44913 MW; 0F1E40C3E6594FC4 CRC64;

Query Match 21.0%; Score 260.5; DB 13; Length 403;
Best Local Similarity 29.6%; Pred. No. 6.7e-14;
Matches 71; Conservative 43; Mismatches 91; Indels 35; Gaps 7;

Qy 29 REGSEBDLALHMFRLRFEESTYKRPDTAEQFOEELKFOQALDSRDPVSCAFVYVLA 88
Db 167 RAGSDIDCEKLEKFRSLCFVVRTLRNLIKQIEDVETKRLARDHSALD--CCLVYLS 223
Qy 89 HGRE-----GFLKGEDEMYKLENUFEALNNKNCOLRAKPKVYIIQACRGEORDPG- 140
Db 224 HGQCTSHIQPPGGIYGDGKIPIERIVNFFNGSQCSLKGKPKLFFIQACGGEQKQGF 283
Qy 141 -----ETVSGDEIVMVI---KDSPO---TIPTYDALHVSSTVEGYIAYRH 180
Db 284 EVDSESPQDTCRSISDAILPQAPSGNDEPDVAVSLPPIGDIIVSYTFPPGVSRD 343
Qy 181 DQKSCFIQTLVDVFTRKGHILELLEVTTRMAEALVQEGKARKTNPEIQSTLRKRLY 240
Db 344 KVGSGWVVEL-DSVLBHYARSEDLTLKLR---VSDIVSSKGRYKQIPGCFNLRKXIF 399

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Search completed: February 26, 2003, 12:20:28  
 Job time : 26.0319 secs

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GenCore version 5.1.3  
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OM protein - protein search, using SW model

Run on: February 26, 2003, 12:17:35 ; Search time 26.5139 Seconds  
(without alignments)  
877.445 Million cell updates/sec

Title: US-09-989-903-5

Perfect score: 1239

Sequence: 1 MSNPRSLSEEEKYDMSGALAL.....KARKNPDIQSTLRKRLYLQ 242

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	2 JC7517	caspace-14/a - hum
2	293	23.6	452	2 JC6507	caspace-2 - rat
3	289	23.3	435	2 A54821	apoptosis regulato
4	282.5	22.8	277	2 JC5410	CPP32 protein - mo
5	280.5	22.6	277	2 S64710	cysteine proteinas
6	272.5	22.0	277	2 A55315	cysteine proteinas
7	264.5	21.3	454	2 JC7123	caspace-9 long cha
8	248.5	20.1	503	2 A49429	interleukin-1 beta
9	246.5	19.9	212	2 I67437	cysteine proteinas
10	239.5	19.3	416	2 G02635	ICE-LAP6 - human
11	230	18.6	495	2 T20038	hypothetical prote
12	226	18.2	311	2 B56084	interleukin-1 beta
13	226	18.2	383	2 A56084	interleukin-1 beta
14	226	18.2	404	2 A42677	interleukin-1 beta
15	225	18.2	418	2 B57511	interleukin-1 beta
16	217.5	17.6	402	2 A46495	IL-1 beta converta
17	213.5	17.2	482	2 I67436	interleukin-1 beta
18	210.5	17.0	826	2 T43638	caspace-related pr
19	207	16.7	263	2 C56084	interleukin-1 beta
20	205.5	16.6	377	2 A57511	interleukin-1 beta
21	197	15.9	312	2 B54821	apoptosis regulato
22	189	15.3	536	2 T43633	caspace-related pr
23	185	14.9	488	2 T13385	hypothetical prote
24	174.5	14.1	642	2 T27021	hypothetical prote
25	159.5	12.9	136	2 I53300	interleukin-1 beta
26	103.5	8.4	1313	2 A48467	myosin heavy chain
27	98	7.9	1957	2 A45627	myosin heavy chain
28	97.5	7.9	139	2 T43642	caspace protein 3
29	97	7.8	1051	2 T18302	apB protein - Eme

30	95.5	7.7	1190	2 B84193	chromosome segrega
31	95.5	7.7	2104	2 T38774	myosin-3 heavy cha
32	95	7.7	761	2 E82205	chemotaxis protein
33	91	7.3	394	2 T26968	hypothetical prote
34	91	7.3	510	2 S42626	BR-golgi intermedi
35	90.5	7.3	520	2 F70350	recombination prot
36	89.5	7.2	467	2 D95253	L-fuculose kinase
37	89.5	7.2	482	2 B98118	thamulokinase (EC
38	89.5	7.2	1225	2 A56514	chromokinesin - ch
39	89	7.2	352	2 G71328	probable flagellar
40	88.5	7.1	149	2 T43637	caspace protein 1C
41	88.5	7.1	661	2 B97733	excinuclease ABC s
42	88.5	7.1	858	1 IJRTNC	neural cell adhesi
43	88.5	7.1	1203	2 B55094	chromosomal protei
44	88.5	7.1	2954	2 T14156	kinasin-related pr
45	88	7.1	505	2 S39520	H+-transporting tw

## ALIGNMENTS

## RESULT 1

JC7517

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C:Accession: JC7517

R: Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A:Title: Caspace-14: Analysis of gene structure and mRNA expression during keratinocyte

A:Reference number: JC7517; MIM:20517231; PMID:11062009

A:Contents: Epidermal keratinocytes

A:Accession: JC7517

A:Molecule type: mRNA

A:Residues: 1-242 <ECK>

A:Cross-references: GB:AF097874

C:Comment: This enzyme accumulates during keratinocyte differentiation and is activated

C:Genetics:

A:Gene: caep-14/a

A:Map position: 19p13.1

A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C:Keywords: differentiation

Query Match 99.6%; Score 1234; DB 2; Length 242;  
Best Local Similarity 99.6%; Pred. No. 1.1e-88;  
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALBHMFRQLRPESTMKDPTAEQ	60
DB	1	MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALBHMFRQLRPESTMKDPTAEQ	60
QY	61	FOBLEKFOQALIDREDPVSCAFVLMAGREGFLKEDGEMVLEULFELNNKNCQAL	120
DB	61	FOBLEKFOQALIDREDPVSCAFVLMAGREGFLKEDGEMVLEULFELNNKNCQAL	120
QY	121	RAKRVYTIQACRGEOBPDGFTVGDEIVMYIKDSPOTIPYTDALHYSTVEGVAYRH	180
DB	121	RAKRVYTIQACRGEOBPDGFTVGDEIVMYIKDSPOTIPYTDALHYSTVEGVAYRH	180
QY	181	DQKSCFIQTLVDVFTYRKGHILELTVTRMAEAEIVGKARKTNPEIQSTLRKRLY	240
DB	181	DQKSCFIQTLVDVFTYRKGHILELTVTRMAEAEIVGKARKTNPEIQSTLRKRLY	240
QY	241	LQ 242	
DB	241	LQ 242	

## RESULT 2

JC6507

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000

C:Accession: J06507  
 R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.  
 Gene 202, 127-132, 1997  
 A:Title: Cloning and expression of the cDNA encoding rat caspase-2.  
 A:Reference number: J06507; MUID:98087427; PMID:9427555  
 A:Accession: J06507  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-452 <SAT>  
 A:Cross-references: GB:U77933; NID:92769705; PID:AB96379.1; PID:92769706

Query Match 23.6%; Score 293; DB 2; Length 452;  
 Best Local Similarity 31.5%; Pred. No. 3e-15;  
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

Oy 29 REGSEDDALAHMFRQLFESTMKRDPFAEQFOELKFOALDSREDPVSCAFVYMA 88  
 Db 219 RGGGVDTHTLTFLGLGVNHLVDQTAQEQEKLQNFQAQ-LPHARVTDSC-IVALLS 276  
 Oy 89 HREGFLKGEDEEMVYKLELFEALNNKNCQALRAKPKYIIQACRGEORDPG----- 140  
 Db 277 HVEGGIVVDGKLTQLQGVFRLFDNANCPSONKPKMFIIQCRGDETRGVDOODGKN 336  
 Oy 141 -----ETVGGDEIVWYIKDSPQTIPTYTALHYSTVEGYIAYRHODKSCFIQTLV 192  
 Db 337 HAQSPGCESSDAGKEBELMKR-----LPTRSDMICGYACLKGNAAARNTKRGSWYIEALT 391  
 Oy 193 DVFTKR--KGHLELLETVTRMAEALVQEGKARKTN-----PEIOTLRKRLYL 241  
 Db 392 QVFSEBACMHVADMLVKVNALIKD---REGVAPGTEFHRCKEMSEYSTLCQOLYL 445

# RESULT 3

A54821  
 Apoptosis regulator ICH-1, stimulatory form L - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
 C:Accession: A54821  
 R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.  
 Cell 78, 739-750, 1994  
 A:Title: ICH-1, an I $\kappa$ B/c $\kappa$ B-3-related gene, encodes both positive and negative regulators  
 A:Reference number: A54821; MUID:94373811; PMID:8087842  
 A:Accession: A54821  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-435 <WAN>  
 A:Cross-references: GB:U13021; NID:9537291; PID:9537292  
 C:Keywords: alternative splicing; apoptosis

Query Match 23.3%; Score 289; DB 2; Length 435;  
 Best Local Similarity 31.1%; Pred. No. 5.8e-15;  
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

Oy 29 REGSEDDALAHMFRQLFESTMKRDPFAEQFOELKFOALDSREDPVSCAFVYMA 88  
 Db 202 RGGGVDTHTLTFLGLGVNHLVDQTAQEQEKLQNFQAQ-LPHARVTDSC-IVALLS 259  
 Oy 89 HREGFLKGEDEEMVYKLELFEALNNKNCQALRAKPKYIIQACRGEORDPG----- 140  
 Db 260 HVEGGIVVDGKLTQLQGVFRLFDNANCPSONKPKMFIIQCRGDETRGVDOODGKN 319  
 Oy 141 -----ETVGGDEIVWYIKDSPQTIPTYTALHYSTVEGYIAYRHODKSCFIQTLV 192  
 Db 320 HAQSPGCESSDAGKE-----KLPRKRLPTRSDMICGYACLKGNAAARNTKRGSWYIEALT 374  
 Oy 193 DVFTKR--KGHLELLETVTRMAEALVQEGKARKTN-----PEIOTLRKRLYL 241  
 Db 375 QVFSEBACMHVADMLVKVNALIKD---REGVAPGTEFHRCKEMSEYSTLCRHLYL 428

RESULT 4  
 J05410  
 CPP32 protein - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 10-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 17-Mar-1999  
 C:Accession: J05410  
 R:Murakami, T.; Urae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.  
 Biochem. Biophys. Res. Commun. 231, 770-774, 1997  
 A:Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation  
 A:Reference number: J05410; MUID:97224429; PMID:9070890  
 A:Accession: J05410  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-277 <MKU>  
 A:Cross-references: DDBJ:D86352  
 A:Experimental source: embryo  
 C:Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 22.8%; Score 282.5; DB 2; Length 277;  
 Best Local Similarity 32.4%; Pred. No. 1.1e-14;  
 Matches 81; Conservative 38; Mismatches 104; Indels 27; Gaps 8;

Oy 9 BEKYMSGALALILCVT-----KAREGSEDDALAHMFRQLFESTMKRDPFA 58  
 Db 34 DSYKMDYPEMGICITITNKFNHSTGMSRSGTDVDAAALRETFMGLKYEVRKNKDLTR 93  
 Oy 59 EPOFELKFOQALDSREDPVSCAFVYMAHGREGFLKGEDEEMVYKLELFEALNNKNCQ 118  
 Db 94 BEIMELMDSVSKEDHSKSSFC---VILSHGDEGVIFGTNGP-VDLKLTSPFRGDCYR 149  
 Oy 119 ALRAKPKYIIQACRGEORDPG-ETVGGDEIVWYIKDSPQTIPTYTALHYSTVEGYIA 177  
 Db 150 SLTGPKPKFIITQACRGTLDGIEITDSGTDEMAC---QKIPEVADPLVYSTAPGYYS 205  
 Oy 178 YRHODKSCFIQTLVDVFTKRKHILE--LLETVTRMA-----EAEVQEGKARKTNPE 230  
 Db 206 WRNSKDGSMFIQSLCSML-KLYAHKLEFMHILITRNKRVALEFESFSDSTFHAKQIPC 264  
 Oy 221 IOSTLRKRLYL 240  
 Db 265 IVSMILTKEYL 274

# RESULT 5

S64710  
 cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster  
 C:Species: Cricetus griseus (Chinese hamster)  
 C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
 C:Accession: S64710; S72395  
 R:Wang, X.; Zelenek, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.  
 EMBO J. 15, 1012-1020, 1996  
 A:Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during  
 A:Reference number: S64710; MUID:96183185; PMID:8605870  
 A:Accession: S64710  
 A:Status: nucleic acid sequence not shown

A:Residues: 1-277 <WAN>  
 A:Molecule type: mRNA  
 A:Cross-references: EMBL:U27463  
 submitted to the EMBL Data Library, May 1995  
 A:Reference number: S72395  
 A:Accession: S72395

A:Residues: 1-79, 'A', '81-146', 'Y', '148-277 <WAW>  
 A:Molecule type: mRNA  
 A:Cross-references: EMBL:U27463; NID:91244443; PID:91244444  
 C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 22.6%; Score 280.5; DB 2; Length 277;  
 Best Local Similarity 35.9%; Pred. No. 1.6e-14;  
 Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

Oy 29 REGSEDDALAHMFRQLFESTMKRDPFAEQFOELKFOALDSREDPVSCAFVYMA 88  
 Db 64 RSGTVDAAKRLRETFMNLKYEVRKNKDLREITVELMKNASKEDHSKSSFC---VILS 120  
 Oy 89 HREGFLKGEDEEMVYKLELFEALNNKNCQALRAKPKYIIQACRGEORDPG-ETVGGDE 147



Db	121	HGDGEVIFGTGCP--IDLKULSYRGDRGRSLIGKPKLFIQAARGELBDOGIEITDSGTE	179
Oy	148	IVMWIKOSPQIPIPYTDALHVSVEVEGYIAVRHDOKSCFIQTLVDVFTYRKGHILE--	204
Db	180	DDMTC----QKIPEADFLVAYSTAPGVYSWRNPKDSSMFIQSLCSML-KLYAHKLEFMH	234
Oy	205	LLTEVTRMA----EAEIVQSGKARKTNPEQISFLRRLV	240
Db	235	ILTRVNRKVATEEFESFSLDSTFFNAKKQIPCLVSMILTELY	274

RESULT 6  
A55315

cysteine proteinase (EC 3.4.22.-) Cpp32 precursor - human  
 N:Alternate names: cysteine proteinase Cpp32  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Feb-1995 #sequence revision.06-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: A55315; S58899; I39005  
 R:Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.  
 J. Biol. Chem. 269, 30761-30764, 1994  
 A:Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans  
 A:Reference number: A55315; MUID:95074098; PMID:7983002  
 A:Accession: A55315  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-277 <PER>  
 A:Cross-references: GB:U13737; NID:G561665; PIDN:AAA65015.1; PID:G561666  
 R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.;  
 Yu, V.L.; Miller, D.K.  
 Nature 376, 37-43, 1995  
 A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian  
 A:Reference number: S58899; MUID:95319529; PMID:7596430  
 A:Accession: S58899  
 A:Molecule type: protein  
 A:Residues: 29-46;176-189, 'E',191-193 <NIC>  
 R:Twari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poitier  
 Cell 81, 801-809, 1995  
 A:Title: Yama/Cpp32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease t  
 A:Reference number: A56924; MUID:95292347; PMID:774019  
 A:Accession: I39005  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-189, 'E',191-277 <RES>  
 A:Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA4929.1; PID:9857566  
 #keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match	22.0%;	Score 272.5;	DB 2;	Length 277;
Best Local Similarity	31.9%;	Pred. No. 6.5e-14;		
Matches 80;	Conservative 39;	Mismatches 103;	Indels 29;	Gaps 9;

QY 9 EKKIDMSGAALATALLICVTK-----AEGGEEDIDLAEHHFROLRFSPSTKGRPTA 58  
Db 34 DNSTKMDYPEMGGLCIITNNKKFPHASTGTGTSAGSDVDAAALRETRFNULKYEVRNKNDLTR 93  
QY 59 EQFOEELKFOAALDSREDPVSCAFVVLMAHGREGLKGEDG---EMVKLENTPEALNNKN 116  
Db 94 EEIYELMKDVSKEHDSKRSFVC---VLLSHGEGIIIFGTNGPVLDKKTNFF---RGDR 147  
QY 117 COALRAKPKVYIIQACRGEQRPG-ETVYGDEIYMWIKDSFQTIPTYTDLAHVSTVEGY 175  
Db 148 CRSLTGKPKELIIQACRGTELDGIETSDGYDDMAC---HKIPVADPELYASTAPGY 203  
QY 176 IAYHHDOGSGEFTIYLVDFTK--RKGHILELLLEVRMM--EALVQ---EGGARATNP 229  
Db 204 YSMRNSKDGSMFFISLCMLKQYADKLEFMHILIRVNKKATBESGSPDATPHAKQIP 263

Db 264 CIVSMLTKELY 274

## RESULT 7

JC7123  
 caspase-9 long chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
 C:Accession: JC7123  
 R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.  
 Biochem. Biophys. Res. Commun. 264, 550-555, 1999  
 A>Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9  
 A:Reference number: JC7123; MUID:20001956; PMID:10529400  
 A:Accession: JC7123  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <FUJ>  
 A:Cross-references: DDBJ:AB019600; NID:G6440941; PID:G6440942

Query Match	21.3%	Score 264.5;	DB 2;	Length 454;
-------------	-------	--------------	-------	-------------

Matches 76; Conservative 36; Mismatches 89; Indels 47; Gaps 7;

Qy 29 REGSEEDDALEHMPROLRFESTIMKRDPTIABQ---FOEELKFOAIDSREDPVSCAFV 84

85 VMAHGE-----GFLKGEDEWKLNLFEALNNKNCALRAKPKYIIIOACRGEOR 137

Db 271 VILSHGQASHLQEPGAVYGTDCGSVSIEKI VNI FNGSGCPSLGKPKLFIQACGGEQK 330

331 DHGEVACTSSGERTLDSDSEDPATPEOGGPRPLDQIDAVSLPTPSDILVSYSTPEGFFV 390

QY 177 AYRHQKSCFIQTLVDVFYK--RKGHLELLTEVTRMAEAEVLVOEGKARKTNEPIQST 234

```

DB 391 SWRDKKSGSWYIEIUDGILFQWARSBDJSLLLKV-----ANAVSEKGIYKQIPGCFN 444
000 335 TRKBT VIO 343

```

Db 445 L R K K L F F K 452

## RESULT 8

interleukin-1 beta-converting enzyme homolog CED-3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*

C:Accession: A49429; T37312  
R:Yuan, J.; Shahan, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.

**A>Title:** The *C. elegans* cell death gene *ced-3* encodes a protein similar to mammalian *ice*  
**A:Reference number:** A49429; MUID:94061982; PMID:8242740

A:Molecule type: DNA

A: Cross-references: GB:129052; NID:g6503232; PIDN:AAA27982.2; PID:g650323233  
A/RESIDUES: 1-303 (100%)  
A/Note: sequence extracted from NCBI backbone (NCBITN:139825 NCBIRP:139826)

A;Accession::13/312  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA

A/Residues: 1-417, 'R', 419-503 <YU2>  
A/Cross-references: EMBL:L29052; PIDN:AAA27982.1

A;Gene: ced-3  
A;Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match	20.1%;	Score 248.5;	DB 2;	Length 503;
Best Local Similarity	27.9%;	Pred. No. 9.7e-12;		

QY 29 REGSEEDDALEHMFRLPRESTMKRDPPTAEQFOEELKFOAIDSREDPVSCAPVVLMA 88

Db 259 RNGTHADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRDFAK---HESHGDSALIVLS 314

```

Oy      89  HGRSEFLGGESEAWKLEMLFEALNNKNOQALRAAPKYIIIOAGGGEORDEPEYV----- 143
Db      315 HGEENVIIIGVDDIPISTHEIITDLNANAPRLANKPKIVFVQAGGERDNGFPVLDSDV 374
Oy      144 -----GGEIVNVVIXDSP-----QTIPYTDALHYSTVEGYIAYR 179
Db      375 GVPAPFARLRGMDN-----RDGFLFNFLGCVRPQVQGVWRKKRPSQADIIILAVATTAQYVSMR 429
Oy      180 HDQKSSCFIQTILVDVFT--KRKGHILELLETVTRMAEALVQEG-KARKINPEIQSLTR 236
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      430 NSARGSWFIQAVCEVFSTHAKMDVLELTVENKRVACGFQTSQGSNIIKKQEMPTSRLL 489
Oy      237 KRLY 240
           | : |
Db      490 KKFY 493

RESULT 9
167437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I67437
R:Flaws, J.A.; Kung, K.; Tybovich, A.M.; DeSanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tilly, K.I.
Endocrinology 136, 5042-5053, 1995
nuloa cells of the ovarian follicle.
A:Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cells
A:Reference number: 153300; MUID:96042508; PMID:7588240
A:Accession: I67437
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <RES>
A:Cross-References: EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004371
C:Keywords: cysteine proteinase; hydrolase

```

Query Match	19.9%	Score 246.5	DB 2	Length 212
Best Local Similarity	31.5%	Pred. No. 4.9e-12		
Matches 69	Conservative 34	Mismatches 89	Indels 27	Gaps 8

```

OY      9  EKKMSGAALLILCVT-----KARBSSEEDLALHEMFQALRESIMKDDPPA  58
Db      5  DSSYKNDYDEWEGCITIIINKNKPHKSTGMSARNSTDVDANLRETFPALKYEVANKNDLTR  64
OY      59  EPOEBELERFOOALDSEREDPVSCAFVILMAHGREGEFLKEDGEGMYKLELFEALINKNQ  118
Db      65  EIMELMDSVSKEDHKKRSSFVC---VILSHGBGVIFGNIG-VDLKLITSPFRDXYCR  120
OY      119  ALPAKPKVYIIQACRGEQDPG-ETVGG--DEIVMWIKOSPOTIPYTDALHYSTVEGY  175
Db      121  SLTGPKLFIIOACRGTELDGSIETSGADDDVAC-----QKKPEADFLVYASAPGY  174
OY      176  IAYRHQKSGSCFQTLVDVFTKRKHILE---LLEVTYR  211
Db      175  YSMRNSRGGSWFQSLC-AMLKUYAKLEMHMLLTRNR  212

```

```

RESULT 10
G02635
ICE-LAP6 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #ext_change 05-Nov-1999
A:Accession: G02635
R:Duan, H.; Orth, K.; Chinaiyan, A.M.; Polier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
submitted to the EMBL Data Library, April 1996
A:Reference number: H01513
A:Accession: G02635
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-416 <DUA>
A:Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027

Query Match      19.3%; Score 239.5; DB 2; Length 416;
Best Local Similarity 28.7%; Pred. No 3..9e-11;

```

	Matches	72;	Conservative	46;	Mismatches	84;	Indels	49;	Gaps	9;
QY	27	KAR	ESSE	ED	DL	AL	EM	F	Q	L
Db	178	R	R	T	T	S	N	I	D	E
QY	85	V	L	M	A	G	R	E		
Db	233	V	L	S	H	G	A	S	H	L
QY	138	D	P	G						
Db	293	D	H	G	F	V	A	S	T	S
QY	172	V	E	G	T	A	V	E	R	H
Db	348	P	E	G	F	V	S	W	M	D
QY	232	Q	S	T	L	K	K	L	I	L
Db	404	F	N	F	L	R	K	L	F	F

RESULT 11  
T20038  
hypothetical protein C48D1.2 - *Caenorhabditis elegans*  
C.Species: *Caenorhabditis elegans*  
C.Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #ext\_change 15-Oct-1999  
C.Accession: T20038  
R.Burton, J.  
submitted to the EMBL Data Library, October 1996  
A.Reference number: Z19214  
A.Accession: T20038  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: DNA  
A.Residues: 1-495 <full>  
A.Cross-References: EMBL:Z61049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2  
A.Experimental source: clone C48D1

A:Gene: CESP:C48D1.2  
A:Map position: 4  
A:introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

[illegible]

RESULT 12  
B56084  
interleukin-1beta converting enzyme gamma isozyme - human  
C.Species: Homo sapiens (man)  
C.Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 05-Nov-1999  
C.Accession: B56084  
R.Alnemiri, E.S.; Fernandes-Alnemiri, T.; Litwack, G.  
J. Biol. Chem. 270, 4312-4317, 1995  
A.Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver



Db 128 IAFCSSTPDNYSWRHPTMWSVFIGRLIE-----HMOEYACSDVEEIFRKVRFSFEQP 380  
 QY 221 EGRKARTNPEIOSTLRKRLYL 241  
 Db 381 DGRQMPTTE-RVLTTRCFYL 400

## RESULT 15

B57511  
 interleukin-1 beta converting enzyme (EC 3.4.22.-) ICE-rel-III - human  
 C/Species: Homo sapiens (man)  
 C/Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 01-Dec-2000  
 C/Accession: B57511; S62183  
 R/Munday, N.A.; Vailancourt, J.P.; Ali, A.; Casano, F.J.; Miller, D.K.; Molineaux, S.M.;  
 J. Biol. Chem. 270, 15870-15876, 1995  
 A/Title: Molecular cloning and pro-apoptotic activity of ICE-relII and ICE-relIII, membe  
 A/Reference number: A57511; MUID:95318183; PMID:7797592  
 A/Accession: B57511  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-418 <MUN>  
 A/Cross-references: GB:U28015; NID:g975300; PIDN:AA475172.1; PID:g903936  
 R/Faucheu, C.; Blanchet, A.M.; Collard-Dutilleul, V.; Lalanne, J.L.; Du-Hercend, A.  
 Eur. J. Biochem. 236, 207-213, 1996  
 A/Title: Identification of a cysteine protease closely related to interleukin-1-beta-con  
 A/Reference number: S62183; MUID:96184899; PMID:8617266  
 A/Accession: S62183  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 55-317; L, 319-418 <FAU>  
 A/Cross-references: EMBL:X94993; NID:g1155085; PIDN:CAA4450.1; PID:g1155086  
 C/Keywords: cysteine proteinase; hydrolase

Query Match 18.2%; Score 225; DB 2; Length 418;  
 Best Local Similarity 26.8%; Pred. No. 5.2e-10;  
 Matches 68; Conservative 53; Mismatches 85; Indels 48; Gaps 10;

QY 19 LALILCVTK-----AREGSEEDLDLEHMFROLPFESTWKRDPTEAQFOELEKFCQALD 73  
 Db 178 LALILCNKTFDLPRANGAHYDIVGMRLLQGLGYVDEKULIARDMESVLRFAFRPE 237  
 QY 74 SREDPVSCAFVVLMAHG-REGFL---KGEDEMYKLENIPEALNNKNCQALRAKPKYI 128  
 Db 238 HKSS--DSTFLVLMHGILEGICGTAHKKKKPPDLVLTIFQIPNNRNCLSLKDKPKVII 295  
 QY 129 IOACRGEPQDPGETVGGDEIVNVIKDSPQTIPTT-----DALHY 169  
 Db 236 VOACRGEKH-GE-----LWVRDSPASLAVISSQSSSENLEADSVCKIHEKDFIAC 345  
 QY 170 STVEGIAYRHQKSCFIQTLVDVFTKRK--GHILELTVETRRMAEALVQEGKARKT 227  
 Db 346 STPHNVSRDRTRGSIPTTELITCFQKYSCCCHMEIF---RKVQKSFVFPQAKQMP 401  
 QY 228 NPEIOSTLRKRLYL 241  
 Db 402 TIE-RATLTDFYL 414

Search completed: February 26, 2003, 12:21:31  
 Job time : 27.5139 secs



PI Alnemri ES, Fernandez-Alnemri T;  
XX  
DR WPI: 2000-376558/32.  
DR N-PSDB; AAA15164.  
XX  
PT Novel nucleic acids encoding cell death specific protease termed  
PT caspase-14 useful for treating cancers by stimulating apoptosis -  
XX  
PS Claim 13; Fig 7; 78pp; English.  
XX  
CC The present sequence represents a human caspase-14 polypeptide. The  
CC polypeptide is a cell death specific protease, and is an apoptosis  
CC stimulator. Caspase-14 polynucleotides and polypeptides, and  
CC anti-caspase-14 antibodies are useful for treating or reducing the  
CC severity of pathological conditions associated with increased or  
CC decreased levels of apoptosis. Apoptosis mediated diseases such as  
CC AIDS, neurodegenerative diseases and ischemic injury are treated by  
CC administering anti-caspase-14 antibodies. The antibody is useful for  
CC determining the presence or the level of caspase-14 in tissue sample  
CC and also for the isolation of caspase-14 with apoptotic activity or  
CC in screening assay to identify an agent that inhibits heterodimer or  
CC heterotrimer formation and therefore, apoptosis.  
XX  
SQ Sequence 242 AA;  
Query Match 99.6%; Score 1234; DB 21; Length 242;  
Best local similarity 99.6%; Pred. No. 1.9e-121;  
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60  
DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60  
QY 61 FOEELKFOQALDSREDPVSCAFVLMAGRGEGFLKGEDEGVKLENLFEALNNKNCQAL 120  
DB 61 FOEELKFOQALDSREDPVSCAFVLMAGRGEGFLKGEDEGVKLENLFEALNNKNCQAL 120  
QY 121 RAKPKVYIIIOACRGQRDPGEIVGDEIWMVTKDSPTIPTYTDALHYSTVEGYIAYRH 180  
DB 121 RAKPKVYIIIOACRGQRDPGEIVGDEIWMVTKDSPTIPTYTDALHYSTVEGYIAYRH 180  
QY 181 DQKGSCTIQLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240  
DB 181 DQKGSCTIQLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240  
QY 241 LQ 242  
DB 241 LQ 242  
RESULT 2  
AAAG77980  
ID AAG77980 standard; Protein; 242 AA.  
XX  
AC AAG77980;  
XX  
DT 05-APR-2002 (first entry)  
XX  
DE Full-length human caspase-14.  
XX  
KW Human; caspase-14; anti-apoptotic; apoptosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200181595-A2.  
XX  
PD 01-NOV-2001.  
XX  
PE 27-APR-2001; 2001WO-US13831.  
XX  
PR 27-APR-2000; 2000US-19962P.  
XX  
PA (KNOL) KNOLL GMBH.

XX  
PI Mankovich JA;  
XX  
DR WPI: 2002-041410/05.  
DR N-PSDB; AAK96248.  
XX  
PT Novel isolated human caspase-14 proteins and nucleic acid sequences,  
PT useful for identifying modulators of caspase-14 protein that are useful  
PT for modulating apoptosis -  
XX  
PS Claim 20; Fig 1; 58pp; English.  
XX  
CC The sequence represents the novel full-length human caspase-14 protein,  
CC referred to as "Caspase-14 NEW" in the specification. The invention  
CC relates to a novel isolated human caspase-14 protein comprising an amino  
CC acid sequence with MSNPRSLSE, at its amino terminus. The caspase-14 of  
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator  
CC of caspase-14 activity. The polypeptide is useful for identifying a  
CC compound which is a modulator of human caspase-14 activity, and is also  
CC useful for identifying a target molecule. An antibody to caspase-14 is useful  
CC for isolating the protein by standard techniques, and for detecting  
CC caspase-14 to evaluate the abundance and expression pattern. The antibody  
CC is also useful for diagnostically monitoring protein levels in a tissue  
CC as a part of a clinical testing procedure. The polypeptide is useful as a  
CC protease to cleave substrates and for inducing apoptosis in cells, in  
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid  
CC assay to identify other proteins that interact with human caspase-14  
XX  
SQ Sequence 242 AA;  
Query Match 99.6%; Score 1234; DB 23; Length 242;  
Best local similarity 99.6%; Pred. No. 1.9e-121;  
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60  
DB 1 MSNPRSLSEEEKYDMSGARLALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPTEAQ 60  
QY 61 FOEELKFOQALDSREDPVSCAFVLMAGRGEGFLKGEDEGVKLENLFEALNNKNCQAL 120  
DB 61 FOEELKFOQALDSREDPVSCAFVLMAGRGEGFLKGEDEGVKLENLFEALNNKNCQAL 120  
QY 121 RAKPKVYIIIOACRGQRDPGEIVGDEIWMVTKDSPTIPTYTDALHYSTVEGYIAYRH 180  
DB 121 RAKPKVYIIIOACRGQRDPGEIVGDEIWMVTKDSPTIPTYTDALHYSTVEGYIAYRH 180  
QY 181 DQKGSCTIQLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240  
DB 181 DQKGSCTIQLVDVFTKRGHILELLEVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240  
QY 241 LQ 242  
DB 241 LQ 242  
RESULT 3  
AAAG77984  
ID AAG77984 standard; Protein; 242 AA.  
XX  
AC AAG77984;  
XX  
DT 05-APR-2002 (first entry)  
XX  
DE Full-length human caspase-14 old.  
XX  
KW Human; caspase-14; anti-apoptotic; apoptosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200181595-A2.  
XX

Accession	Protein Name	Species	Length (AA)	Score	DB	Length (aa)	Score	DB
PD01-NOV-2001.			242	96.0%	1189	23	242	
XX27-APR-2001; 2001WO-US13831.			242	96.0%	1189	23	242	
XX27-APR-2001; 2001WO-US13831.			242	96.0%	1189	23	242	
PR27-APR-2000; 2000US-199962P.			242	96.0%	1189	23	242	
XX(KNOL ) KNOLL GMBH.			242	96.0%	1189	23	242	
XXMankovitch JA;			242	96.0%	1189	23	242	
XXWPI; 2002-041410/05.			242	96.0%	1189	23	242	
PTNovel isolated human caspase-14 proteins and nucleic acid sequences,			242	96.0%	1189	23	242	
PTuseful for identifying modulators of caspase-14 protein that are useful			242	96.0%	1189	23	242	
PTfor modulating apoptosis -			242	96.0%	1189	23	242	
PSExample; Fig 1; 58pp; English.			242	96.0%	1189	23	242	
XXThe sequence represents the full-length human caspase-14 protein,			242	96.0%	1189	23	242	
XXreferred to as "Caspase-14 OLD" in the specification. The invention			242	96.0%	1189	23	242	
XXrelates to a novel isolated human caspase-14 protein comprising an amino			242	96.0%	1189	23	242	
XXacid sequence with MSNPSTSE, at its amino terminus. The caspase-14 of			242	96.0%	1189	23	242	
XXthe invention has anti-apoptotic activity. Caspase-14 acts as a modulator			242	96.0%	1189	23	242	
XXof caspase-14 activity. The polypeptide is useful for identifying a			242	96.0%	1189	23	242	
XXcompound which is a modulator of human caspase-14 activity, and is also			242	96.0%	1189	23	242	
XXuseful for identifying a compound which modulates the interaction of			242	96.0%	1189	23	242	
XXcaspase-14 with a target molecule. An antibody to caspase-14 is useful			242	96.0%	1189	23	242	
XXfor isolating the protein by standard techniques, and for detecting			242	96.0%	1189	23	242	
XXcaspase-14 to evaluate the abundance and expression pattern. The antibody			242	96.0%	1189	23	242	
XXis also useful for diagnostically monitoring protein levels in a tissue			242	96.0%	1189	23	242	
XXas a part of a clinical testing procedure. The polypeptide is useful as a			242	96.0%	1189	23	242	
XXprotease to cleave substrates and for inducing apoptosis in cells, in			242	96.0%	1189	23	242	
XXscreening assays, and as a bait protein in a two-hybrid or three-hybrid			242	96.0%	1189	23	242	
XXassay to identify other proteins that interact with human caspase-14			242	96.0%	1189	23	242	
XXprotein.			242	96.0%	1189	23	242	
XXSequence 242 AA;			242	96.0%	1189	23	242	
XXQuery Match 96.0%; Score 1189; DB 23; Length 242;			242	96.0%	1189	23	242	
XXBest Local Similarity 99.6%; Pred. No. 1e-116;			242	96.0%	1189	23	242	
XXMatches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0.			242	96.0%	1189	23	242	
QY10 EKYDMSGALALILCVTKAREGSEEDDLAHEMFRLRESTMKRDPPTAEQFOEELKQ 69			242	96.0%	1189	23	242	
DB10 EKYDMSGARLALILCVTKAREGSEEDDLAHEMFRLRESTMKRDPPTAEQFOEELKQ 69			242	96.0%	1189	23	242	
QY70 QAIDREDDPVSCAFVYVLAHAGREGFLKGGDEGMVYLENFEALNNKNCALRAKPKVYII 129			242	96.0%	1189	23	242	
DB70 QAIDREDDPVSCAFVYVLAHAGREGFLKGGDEGMVYLENFEALNNKNCALRAKPKVYII 129			242	96.0%	1189	23	242	
QY130 QACRGEQDPGETVSGDEIWMVYIKDSPQIIPYTDALHYSTVEGIIAYRHQKSGCFIQ 189			242	96.0%	1189	23	242	
DB130 QACRGEQDPGETVSGDEIWMVYIKDSPQIIPYTDALHYSTVEGIIAYRHQKSGCFIQ 189			242	96.0%	1189	23	242	
QY190 TLVDVFTKRKGHILELLEVTTRMAEALVOEGKARKTNPETIOSTLRKRLYIQ 242			242	96.0%	1189	23	242	
DB190 TLVDVFTKRKGHILELLEVTTRMAEALVOEGKARKTNPETIOSTLRKRLYIQ 242			242	96.0%	1189	23	242	
RESULT 4			242	96.0%	1189	23	242	
ID1AA68865			242	96.0%	1189	23	242	
XXAA68865 standard; Protein; 229 AA.								

XX	WO200004169-A1.
XX	
XX	27-JAN-2000.
XX	
XX	12-JUL-1999; 99WO-EP04939.
XX	
XX	17-JUL-1998; 98EP-0202422.
XX	
XX	(VLAAs-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX	
XX	Van De Craen M, Declercq W, Vandenabeele P, Fiers W;
XX	WPI; 2000-182433/16.
XX	DR. N-PSDB; AA260684.
XX	
XX	New murine and human caspase homologues useful for treating skin
XX	related disorders -
XX	
XX	Claim 2; Page 53-54; 68pp; English.
XX	
XX	The present sequence represents a human caspase-like polypeptide.
XX	The specification also describes a murine caspase-like polypeptide.
XX	Caspases are cysteinyl aspartate-specific proteinases which play a
XX	central role in apoptosis. The polypeptides of the invention are related
XX	to human and murine caspase-2 and human caspase-9, and possess all of
XX	the typical amino acids involved in catalysis, including the QACRG box,
XX	and contain no or only a very short prodomain. mRNA expression of the
XX	homologues of the invention is predominant in the skin. The caspase-like
XX	polypeptides are useful for treating human or animal diseases, such
XX	as skin diseases. They are also useful for screening for compounds that
XX	modulate its activity, i.e. agonists, antagonists, and inhibitors. The
XX	caspase-like polypeptides and polynucleotides are useful for modulating
XX	keratinisation, for diagnosing and treating inappropriate wound
XX	healing.
XX	
XX	Sequence 229 AA;
XX	
XX	Query Match 94.1%; Score 1166; DB 21; Length 229;
XX	Best Local Similarity 99.6%; Pred. No. 2,56-114;
XX	Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX	
QY	14 MSGALALILCVTKAREGSEEDLDALHEMFQRLRFESTMKSDPTAEQFOEELKRFQAI
DB	1 MSGARLAILICVTARKRESEEDLDALHEMFQRLRFESTMKSDPTAEQFOEELKRFQAI
QY	74 SREDPVSQAFVYVLAHAGREGFLKGEDGSMVKLENLFEALNNKNCQALPAKPKVYIIQCR
DB	61 SREDPVSQAFVYVLAHAGREGFLKGEDGSMVKLENLFEALNNKNCQALPAKPKVYIIQCR
QY	134 GEORPGETVGDEIWMYIKDSPOTIPYTDALHYSVVEGVIAYRHQKSCFIQTLYVD
DB	121 GEORPGETVGDEIWMYIKDSPOTIPYTDALHYSVVEGVIAYRHQKSCFIQTLYVD
QY	194 VETKRKGHILELLEVTTRMAEAEIVQEGKARKTNPEIQSTLRKRLYQ 242
DB	181 VETKRKGHILELLEVTTRMAEAEIVQEGKARKTNPEIQSTLRKRLYQ 229
XX	
XX	RESULT 5
XX	ID AAY93216
XX	AAV93216
XX	AAV93216 standard; Protein; 214 AA.
XX	AAV93216;
XX	
XX	04-SEP-2000 (first entry)
XX	
XX	Amino acid sequence of a human caspase-14 splice variant.
XX	
XX	Caspase-14; cell death specific protease; apoptosis stimulator;
XX	apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX	
XX	Homo sapiens.
XX	

XX Key Location/Qualifiers  
 FH Active-site 102..106  
 XX  
 XX WO200028047-A1.  
 XX  
 XX 18-MAY-2000.  
 XX  
 XX 29-OCT-1999; 99WO-US25523.  
 XX  
 XX 06-NOV-1998; 98US-0187789.  
 XX  
 XX (UYUE-) UNIV JEFFERSON THOMAS.  
 XX  
 XX Alnemri ES, Fernandez-Alnemri T;  
 XX  
 XX WPI; 2000-376556/32.  
 XX  
 XX N-PSDB; AAI15166.  
 XX  
 XX Novel nucleic acids encoding cell death specific protease termed  
 PT caspase-14 useful for treating cancers by stimulating apoptosis -  
 XX  
 XX Claim 42; Fig 9; 78pp; English.  
 XX  
 XX The present sequence represents a human caspase-14 splice variant. The  
 CC polypeptide is a cell death specific protease, and is an apoptosis  
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and  
 CC anti-caspase-14 antibodies are useful for treating or reducing the  
 CC severity of pathological conditions associated with increased or  
 CC decreased levels of apoptosis. Apoptosis mediated diseases such as  
 CC AIDS, neurodegenerative diseases and ischemic injury are treated by  
 CC administering anti-caspase-14 antibodies. The antibody is useful for  
 CC determining the presence or the level of caspase-14 in tissue sample  
 CC and also for the isolation of caspase-14 with apoptotic activity or  
 CC in screening assay to identify an agent that inhibits heterodimer or  
 CC heterotetramer formation and therefore, apoptosis.  
 CC  
 XX Sequence 214 AA;  
 SQ

Query Match 86.0%; Score 1065; DB 21; Length 214;  
 Best Local Similarity 88.0%; Pred. No. 9.7e-104;  
 Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKARSGSEEDLDALHMFRLQRFSTWKRDPYAEQ 60  
 Db 1 MSNPRLSEEEKYDMSGARALILCVTKARSGSE----- 34  
 QY 61 FOEIELEKFOQAIDSRDDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120  
 Db 35 --EELEKFOQAIDSRDDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 92  
 QY 121 RAKPRVYIIQACRGORDDGETVSGDEITMVVKDSPPQITPTTDLAHVSTVEGYIAYKH 180  
 Db 93 RAKPRVYIIQACRGORDDGETVSGDEITMVVKDSPPQITPTTDLAHVSTVEGYIAYKH 152  
 QY 181 DQKSGCFIQLTLDVFTFKRGHILLELLETVTRMAEAEALVQEGKARKTNPEIOSTLRKRLY 240  
 Db 153 DQKSGCFIQLTLDVFTFKRGHILLELLETVTRMAEAEALVQEGKARKTNPEIOSTLRKRLY 212  
 QY 241 LQ 242  
 Db 213 LQ 214

RESULT 6  
 AAY68864  
 ID AAY68864 standard; Protein; 257 AA.  
 XX  
 XX AC AAY68864;  
 XX  
 XX 16-MAY-2000 (first entry)  
 XX  
 XX Amino acid sequence of a murine caspase-like polypeptide.

XX KW Mouse; caspase-like polypeptide; human; caspase; apoptosis;  
 KW skin disease; keratinisation; wound healing.  
 XX  
 XX OS Mus musculus.  
 XX  
 XX WO200004169-A1.  
 XX  
 XX 27-JAN-2000.  
 XX  
 XX 12-JUL-1999; 99WO-EP04939.  
 XX  
 XX 17-JUL-1998; 98EP-0202422.  
 XX  
 XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
 XX  
 XX Van De Craen M, Declercq W, Vandenabeele P, Fiers W;  
 XX  
 XX WPI; 2000-182433/16.  
 XX  
 XX N-PSDB; AAZ60683.  
 XX  
 XX New murine and human caspase homologues useful for treating skin  
 PT related disorders -  
 PT  
 XX  
 XX Claim 1; Page 51-52; 68pp; English.  
 XX  
 XX The present sequence represents a murine caspase-like polypeptide. The  
 CC specification also describes a human caspase-like polypeptide.  
 CC Caspases are cysteinyl aspartate-specific proteinases which play a  
 CC central role in apoptosis. The polypeptides of the invention are related  
 CC to human and murine caspase-2 and human caspase-9, and possess all of  
 CC the typical amino acids involved in catalysis, including the QACRG box,  
 CC and contain no or only a very short prodomain. mRNA expression of the  
 CC homologues of the invention is predominant in the skin. The caspase-like  
 CC polypeptides are useful for treating human or animal diseases, such  
 CC as skin diseases. They are also useful for screening for compounds that  
 CC modulate its activity, i.e. agonists, antagonists, and inhibitors. The  
 CC caspase-like polypeptides and polynucleotides are useful for modulating  
 CC keratinisation, for diagnosing and treating inappropriate wound  
 CC healing.  
 CC  
 XX Sequence 257 AA;  
 SQ

Query Match 75.4%; Score 934.5; DB 21; Length 257;  
 Best Local Similarity 70.9%; Pred. No. 7e-90;  
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRLSEEEKYDMSGALALILCVTKARSGSEEDLDALHMFRLQRFSTWKRDPYAEQ 60  
 Db 5 MSNPRLSEEEKYDMSGARALILCVTKARSGSEEDLDALHMFRLQRFSTWKRDPYAEQ 64  
 QY 61 FOEIELEKFOQAIDSRDDPVSCAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 120  
 Db 65 FLEIEDEFOQITIDNNEEVSQAFVVLMAHGREGLKGEDGEMVKLENLFEALNNKNCQAL 124  
 QY 121 RAKPRVYIIQACRGORDDGETVSGDEITMVVKDSPPQITPTTDLAHVSTVEGYIAYKH 168  
 Db 125 RAKPRVYIIQACRGORDDGETVSGDEITMVVKDSPPQITPTTDLAHVSTVEGYIAYKH 183  
 QY 169 YSTVEGYIAYKHDOKSGCFIQLTLDVFTFKRGHILLELLETVTRMAEAEALVQEGKARKTN 228  
 Db 184 YSTVEGYIAYKHDOKSGCFIQLTLDVFTFKRGHILLELLETVTRMAEAEALVQEGKARKTN 243  
 QY 229 PEIOSTLRKRLYLQ 242  
 Db 244 PEVOSTLRKRLYLQ 257

RESULT 7  
 AAW93592  
 ID AAW93592 standard; Protein; 281 AA.  
 XX  
 XX AC AAW93592;  
 XX



Query Match	Best Local Similarity	Score	DB	Length	281
Matches	180;	Conservative	31;	Mismatches	30;
			Indels	13;	Gaps
1	MSNPRLSEEEKYDMSGALALILCTVKAREGSEEDIDALEHMFROUPEFSTMKRDPYAEQ	60			
24	MSDPLQLEERYDMSGARLALTLCTVKAREGSEVEDALEHMFRRYLKFFSTMKRDPYAEQ	83			
61	FOEELKFOALDISEDPPVSCAFVYVMARGRGFLKGEQGVNKLLENLEALANNKKCOAL	120			

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Db      84 FLEEDDEFQOTIDWNEEVSACFVLVLMHAGEGLLKGDENRVLIEDFEVLNNKNCAL 14
Oy      121 RAKPRVVYIIQCRCGRQRPC-----FTVGGEIMVMVKDSPQTIPYTDLAHV 166
         |||:|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      144 RGKPRVVIIOACRGHRPBGELNGEELGDEELGGDE-VAVLKNPNPOS IPTYDTLHI 207
         |||:|||||::|||::|||::|||::|||::|||::|||::|||::|||
Oy      169 YSTGVGYIAYHHDDKGSCFIOTLVDFPTFRKGHLIELLTVEYTRMAAEALVOEGKARKTN 222
         |||:|||||::|||::|||::|||::|||::|||::|||::|||::|||
Db      203 YSTGVGYISTYHDENGSGSFITQLTDVPFHKKGSILBELTEITRLMANTEWNOECKPRKVN 267
         |||:|||||::|||::|||::|||::|||::|||::|||::|||::|||
Oy      229 PEIQSTLRKLRYLQ 242
         |||:|||||::|||::|||::|||::|||::|||::|||::|||::|||
Db      263 FEVOSTLRKLRYLQ 276

RESULT 8
AAV93213
ID AAV93213 standard; Protein; 281 AA.
XX AC AAV93213;
XX DT 04-SEP-2000 (first entry)
XX DE Amino acid sequence of a murine caspase-14.
XX KM Caspase-14; cell death specific protease; apoptosis stimulator;
XX KM apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX OS Mus sp.
XX FH Key
XX FH Region 1..156 Location/Qualifiers
           |note= "large subunit"
FT Active-site 134..138
FT Cleavage-site 156..157
FT Cleavage-site 162..163
FT Region 163..257
          /note= "small subunit"
FT
FN WO200028047-A1.
PN 18-MAY-2000.
PD 29-OCT-1999; 99WO-US2553.
PF 06-NOV-1998; 98US-0187789.
PR
XX (UJYE-) UNIV JEFFERSON THOMAS.
PA Alnemri ES, Fernandez-Alnemri T;
PI WPI; 2000-376558/32.
DR N-PSDB; AAA15163.
DZ
XX Novel nucleic acids encoding cell death specific protease termed -
PT Caspase-14 useful for treating cancers by stimulating apoptosis -
PT Claim 52; Fig 1; 78pp; English.
XX The present sequence represents a murine caspase-14 polypeptide. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14 polynucleotides and polypeptides, and
CC anti-caspase-14 antibodies are useful for treating or reducing the
CC severity of pathological conditions associated with increased or
CC decreased levels of apoptosis. Apoptosis mediated diseases such as
CC AIDS, neurodegenerative diseases and ischemic injury are treated by
CC administering anti-caspase-14 antibodies. The antibody is useful for
CC determining the presence or the level of caspase-14 in tissue sample
CC and also for the isolation of caspase-14 with apoptotic activity or
CC in screening assay to identify an agent that inhibits heterodimer or
CC heterotrimer formation and therefore, apoptosis.
XX Sequence 281 AA;
```



CC disease or disorder selected from cancers (e.g., of tissues, of blood or  
 CC hematopoietic origin, of the breast, colon, lung, prostate, cervical,  
 CC brain, ovarian, bladder or kidney), immune-related diseases and  
 CC disorders, cardiovascular disease, brain or neuronal-associated diseases  
 CC (e.g., central or peripheral nervous system diseases, migraine, pain,  
 CC sexual dysfunction, mood disorders, attention disorders, cognition  
 CC disorders, hypotension, hypertension, psychotic disorders, neurological  
 CC disorders and dyskinesias), metabolic disorders and inflammatory  
 CC disorders. (1) may also be useful as a diagnostic tool for a disease or  
 CC disorder such as those above. AAU72876-AAU72910 represent human  
 CC protease amino acid sequences of the invention.

XX Sequence 234 AA;

Query Match 38.1%; Score 472.5; DB 23; Length 234;

Best Local Similarity 45.0%; Pred. No. 2.7e-41; Mismatches 73; Indels 11; Gaps 7;

Db 1 KYDSGALLALILCVTKAREGSEEDLDALHMFRLQRFESTMKRDPYAEQFQELKRFQ 70  
 1 QYDLSKARAAALLLAVIQGRPGAHQDVEALGICWALGFETTVRTDPTQAQFQELAQPRE 60

Qy 71 AIDREDPVSCAFVLMNH-GREGFLKGEDEMKLENLFEALNNKNCQALRAKRYIT 129  
 61 QLDTCRGVSCALVALMAHGGPRQLLGADGOEVQPEALMQELS--RCQVLQGRKIFLL 118

Qy 130 QACRGQRDPGETVGDDEIVWIK--DSPQITPTDYLHYSTVEGYIAYRHQKSGSCF 187  
 119 QACGGRNDAG--VGPTLAPWYMSLRAKPSVPSHADVLOIYAEQGVANR-DDKGSDF 175

Qy 188 IQTLVDVFTKRGH-IIELLTEVTRMAEALVDE--GKARKNPEIOSTLRKLYIQ 242  
 176 IQTLVEVLRAKPRDLELLTEVNRVRCQEVLTGPDCELRKACLEIRSSLRRLCQ 233

RESULT 11

ABBI0110 ID ABBI0110 standard; Protein; 452 AA.

AC ABBI0110;

DT 26-JUL-2002. (first entry)

DE Mouse caspase 2 protein.

XX Caspase 2; antiense; cytostatic; osteopathic; cerebroprotective;

KM neuroprotective; antilipemic; antiinflammatory; antimicrobial;

KM haematopoietic disorder; bone metabolism disorder; cholesterol disorder;

KM hyperproliferative disorder; cancer; blood disorder; stroke;

KM brain injury; neurodegenerative disease; infection; inflammation;

XX tumour.

XX Mus musculus.

XX WO200224720-A1.

XX 28-MAR-2002.

XX 14-SEP-2001; 2001WO-US28631.

XX 20-SEP-2000; 2000US-0667018.

XX (ISIS-) ISIS PHARM INC.

XX Zhang H, Watt AT;

XX WPI; 2002-351998/38.

XX N-PSDB; ABB58563.

PT New antisense compounds targeted to nucleic acid molecule encoding  
 PT caspase 2, useful for treating diseases or conditions associated with  
 PT caspase 2, e.g. cancer, blood disorders, stroke, brain injury and  
 PT neurodegenerative diseases

XX Example 13; Page 111-113; 146pp; English.

XX The invention relates to a compound 8-50 nucleobases in length targeted  
 CC to a nucleic acid molecule encoding caspase 2, which specifically  
 CC hybridises with and inhibits the expression of caspase 2, or specifically  
 CC hybridises with at least an 8-nucleobase portion of an active site on a  
 CC nucleic acid molecule encoding caspase 2. The activity of antisense  
 CC oligonucleotides of the invention may be described as, cytostatic,  
 CC osteoprotective, cerebroprotective, neuroprotective, antilipemic,  
 CC antiinflammatory and antimicrobial. The antisense compounds are useful  
 CC for treating an animal having a disease or condition associated with  
 CC caspase 2, such as haematopoietic disorder, bone metabolism disorder,  
 CC cholesterol disorder, or a hyperproliferative disorder. These compounds  
 CC may further be used as research reagents and diagnostic, to distinguish  
 CC between functions of various members of a biological pathway, in the  
 CC treatment of a disease or disorder which can be treated by modulating  
 CC the expression of caspase 2, including cancer, blood disorders,  
 CC stroke, brain injury and neurodegenerative diseases. They may also be  
 CC used for prophylaxis, e.g. to prevent or delay infection, inflammation or  
 CC tumour formation. The current sequence represents the mouse caspase 2  
 CC protein.

XX Sequence 452 AA;

Query Match 23.8%; Score 295; DB 23; Length 452;

Best Local Similarity 31.5%; Pred. No. 3.4e-22; Mismatches 75; Indels 36; Gaps 7;

Qy 29 REGSEEDLDALHMFRLQRFESTMKRDPYAEQFQELKRFQADISBEDPVSCAFVIMA 88  
 219 RSGGDVHTTLVTLFKLGYNVHVHIDQTAQEMQKQNFQAQ-LPARHVTDSQ-VALLS 276

Qy 89 HGREGFLKGEDEMKLENLFEALNNKNCQALRAKRYITQACRGQRDPG----- 140  
 277 HGVGGIYGVNCKLQLOEYFRLFDNANCSLQNKPKMFPQACRGQDTEGVDQDQGN 336

Qy 141 -----ETVGDDEIVWIKDSPQITPTDYLHYSTVEGYIAYRHQKSGCFIOTLV 192  
 337 HTQSPGCEBSPAGKEBELMKR-----LPTSDMTCGYALCKGNAMNMTKRGSVIETLT 391

Qy 193 DVFTKR--KGHILELLEVTTRMAEALVDEGKARKTN-----PEIOSTLRRLYI 241  
 392 QVFSERACDMHVDMLVKVNALIKE---REGVAPGEFPHRCXEMSEYCSITLCOOLYL 445

RESULT 12

AAR66771 ID AAR66771 standard; Protein; 435 AA.

AC AAR66771;

DT 13-SEP-1995 (first entry)

DE Human interleukin-1 beta converting enzyme ced 3 homolog Ich-1(L).

KM Human interleukin-1 beta converting enzyme ced 3 homolog; Ich-1(L);

KM oncogene bcl-2; programmed cell death; cancer treatment.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Active-site 301..305

XX WO9500160-A.

XX 05-JAN-1995.

XX 10-JUN-1994; 94WO-US06630.

XX 24-JUN-1993; 93US-0080850.

XX (GENO ) GEN HOSPITAL CORP.

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XX  Miura M, Yuan J;
PI  WPI: 1995-051742/07.
XX  N-PSDB; AAQ79971.
DR  N-PSDB; AAQ79971.
XX  Promoting or preventing programmed cell death in vertebrate cells
PT  - by inhibiting the activity of interleukin-1 beta converting
XX  enzyme.
XX  Example 5; Fig 12A; 116pp; English.
PS  AAQ79971 encodes AAR6771 human interleukin-1 beta converting enzyme
CC  ced 3 homolog Ich-1(l), increasing Ich-1(l)'s enzymatic activity can
CC  promote the programmed cell death of cancer cells (pref. those
CC  overexpressing the bcl-2 oncogene), this can be used as the basis
CC  of a new cancer treatment. Alternatively by reducing Ich-1(l)'s
CC  enzymatic activity programmed cell death can be inhibited, this may
CC  be useful in the development of new cell lines which remain viable in
CC  culture for extended or indefinite periods, independant of growth
CC  factors.
XX  Sequence 435 AA;
SQ  Query Match 23.3%; Score 289; DB 16; Length 435;
    Best Local Similarity 31.1%; Pred. No. 1.4e-21;
    Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

OY  29 REGSEEDDALEHMFROLFESTMKRDPFAEFOELEKFOQAIISREDPVSCAFVYVMA 88
DB  202 RSGGVVDHSTLVTLFKLGYDVHVLCDQTAQEMOEKLNFAQ-LPAHRYVTSC-IVALLS 259

OY  89 HGREGFLKGEDEGVNKLLENFALNNKNCQALRAKPKVYIIQACRGEORDPG----- 140
DB  260 HGVEGAIIVGDKLQLQGVFQLPFNANCPSLQNKPKMFIQACRGEDETDRGVDDQDGN 319

OY  141 -----ETVGGDEIVWVINDSPOTIPYTDALHVSIVGTYIAYRHDOGSCPTIOTLV 192
DB  320 HAGSPGCEESDAGKE----KLPKKRLPTRSDMTCGYACLGTAAMRNTKRGSWYTEALA 374

OY  193 DVFTKR--KGHLELLTEVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
DB  375 QVFSERACDMHVAIDLKLVNVALIKD---REGYAGTEFHRCKEMSEYCSITLCRHLYL 428

RESULT 13
AAR98462
ID  AAR98462 standard; Protein; 435 AA.
XX  AAR98462;
AC  AAR98462;
XX  25-SEP-1996 (first entry)
XX  Human Ice-ced-3 homologue-1L.
XX  Ich-1L; human ICE-ced-3 homologue; programmed cell death;
XX  apoptosis; interleukin-1 beta converting enzyme; gene therapy.
XX  Homo sapiens.
OS  Homo sapiens.
XX  Key Location/Qualifiers
XX  FT 301..305
XX  FT /label= QACRG_active_domain

XX  WO9620721-A1.
XX  11-JUL-1996.
XX  PD 11-JUL-1996.
XX  PE 04-JAN-1996; 96WO-US00177.
XX  PR 04-JAN-1995; 95US-0368704.
XX  PA (GEHO ) GEN HOSPITAL CORP.

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XX  Miura M, Yuan J;
PI  WPI: 1996-333763/33.
XX  N-PSDB; AAT31552.
DR  N-PSDB; AAT31552.
XX  Preventing or promoting programmed cell death in vertebrate cells
PT  comprises inhibiting or increasing the activity of
XX  interleukin-1-beta converting enzyme, or altering expression of
PT  other related genes
XX  Claim 19; Fig 10A; 127pp; English.
PS  A novel human cell death gene, designated Ich-1 (ICE-ced-3
XX  homologue-1), was identified as a new member of the ced-3/ICE family.
CC  Ich-1 is alternatively spliced into 2 different forms. Ich-1L cDNA
CC  (AAT31552) encodes a 435-amino acid protein (AAR98462) that is
CC  homologous to the P20 and P10 subunits of human interleukin-1 beta
CC  converting enzyme (ICE). Ich-1S cDNA (AAT31553) encodes a 312-amino
CC  acid protein (AAR98463) that is a truncated version of Ich-1L that
CC  terminates 21 residues after the QACRG active domain of Ich-1L.
CC  Overexpression of Ich-1L induces Rat-1 fibroblast cells to die in
CC  culture, but overexpression of Ich-1S suppresses Rat-1 cell death.
CC  Ich-1L and Ich-1S are useful in methods of controlling programmed
CC  cell death of vertebrate cells.
XX  Sequence 435 AA;
SQ  Query Match 23.3%; Score 289; DB 17; Length 435;
    Best Local Similarity 31.1%; Pred. No. 1.4e-21;
    Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

OY  29 REGSEEDDALEHMFROLFESTMKRDPFAEFOELEKFOQAIISREDPVSCAFVYVMA 88
DB  202 RSGGVVDHSTLVTLFKLGYDVHVLCDQTAQEMOEKLNFAQ-LPAHRYVTSC-IVALLS 259

OY  89 HGREGFLKGEDEGVNKLLENFALNNKNCQALRAKPKVYIIQACRGEORDPG----- 140
DB  260 HGVEGAIIVGDKLQLQGVFQLPFNANCPSLQNKPKMFIQACRGEDETDRGVDDQDGN 319

OY  141 -----ETVGGDEIVWVINDSPOTIPYTDALHVSIVGTYIAYRHDOGSCPTIOTLV 192
DB  320 HAGSPGCEESDAGKE----KLPKKRLPTRSDMTCGYACLGTAAMRNTKRGSWYTEALA 374

OY  193 DVFTKR--KGHLELLTEVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
DB  375 QVFSERACDMHVAIDLKLVNVALIKD---REGYAGTEFHRCKEMSEYCSITLCRHLYL 428

RESULT 14
AAR90703
ID  AAR90703 standard; Protein; 435 AA.
XX  AAR90703;
AC  AAR90703;
XX  10-APR-1996 (first entry)
XX  Interleukin-1-beta converting enzyme like apoptosis protease-2.
XX  Interleukin-1-beta converting enzyme like apoptosis protease-2.
XX  Interleukin-1-beta converting enzyme like apoptosis protease-2;
XX  ICE-LAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;
XX  Parkinson disease; septic shock; rheumatoid arthritis; head injury;
XX  antitumour; antiviral.
XX  Homo sapiens.
OS  Homo sapiens.
XX  WO9600297-A1.
XX  04-JAN-1996.
XX  PD 04-JAN-1996.
XX  PE 23-JUN-1994; 94WO-US07127.
XX  PR 23-JUN-1994; 94WO-US07127.
XX  PA (GEHO ) GEN HOSPITAL CORP.

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XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Craig AR, Hastings GA, Hudson PL, Kirkness EF, Wei MH;  
 PI MPI; 1996-068881/07.  
 DR N-PSDB; AAT15579.  
 XX  
 XX Interleukin-1 beta converting enzyme like apoptosis protease-1 and  
 PT -2 - controls programmed cell death, used in treatment of  
 PT immunosuppression related disorders, e.g. AIDS and Alzheimer's  
 PT disease  
 PS Claim 1; Fig 2A-C; 58pp; English.  
 XX  
 XX Human interleukin-1-beta converting enzyme like apoptosis protease-2  
 CC (ICE-LAP-2) (AAM90703) is structurally related interleukin-1-beta  
 CC converting enzyme, which is responsible for apoptosis. Recombinant  
 CC ICE-LAP-2 is obtd. by expression of encoding cDNA (AAT15579) in  
 CC prokaryotic or eucaryotic host cells. It is used to treat diseases  
 CC related to abnormally controlled programmed cell death, to control  
 CC vertebrate development and tissue homeostasis, to overcome viral  
 CC infections and to treat immunosuppression-related disorders.  
 CC  
 SQ Sequence 435 AA;  
 XX  
 XX Query Match 23.3%; Score 289; DB 17; Length 435;  
 Best Local Similarity 31.1%; Pred. No. 1.4e-21;  
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;  
 QY 29 REGSEEDLDALEHMFROLFESTMKRDPATQFOELEKFOQADISREDPVSCAFVILMA 88  
 DB 202 RSGGDVHSTLVTLFKLGVGVHVLCDQTADQEMQKLNFAQ-LPAHVTSDC-IVALLS 259  
 QY 89 HGRGFLKGEDEVKLENLEALNNKQCALRAKPVYIIQACRGQRDPG----- 140  
 DB 260 HGVEGATYGVNDGKLQLEVFQLEFDNANCPSLQNKPMFIOACRGDETRDGVQDQDGN 319  
 QY 141 -----ETVGSDEIVWIKDSPTPTPTDYLHVSTVEGYIAYRHDOGSCFIOTLV 192  
 DB 320 HAGSPGCEESDAGE-----KLPRKRLPTRSDMTCGYACLGTAAMNTKSGSWIIEALA 374  
 QY 193 DVFTKR--KGHILELLEVTTRMAEALVOEGKAKTN-----PEIOTLRLKRLYL 241  
 DB 375 QVFSERACDMHIVADMLVKNALIKD---REGVAPGTFFHRCKEMSEYCSITLCHRLYL 428  
 RESULT 15  
 AAM26274  
 ID AAM26274 standard; Protein; 435 AA.  
 XX  
 AC AAM26274;  
 XX  
 DT 14-APR-1998 (first entry)  
 XX  
 DE Cell death protein ICH-11.  
 XX  
 XX cell death; ICH-11; interleukin-1 beta; apoptosis; treatment;  
 KW IL-1; tumour; oncogenic transformation; IL-1 receptor antagonist;  
 KW IL-1Ra; IL-1 beta.  
 XX  
 XX Homo sapiens.  
 OS  
 PN MO9733606-A1.  
 PD 18-SEP-1997.  
 XX  
 PD 15-MAR-1996; 96WO-US03468.  
 PF  
 XX 15-MAR-1996; 96WO-US03468.  
 PR  
 XX (GEHO) GEN HOSPITAL CORP.  
 PA  
 XX

PI Friedlander R, Yuan J;  
 XX  
 XX MPI; 1997-470641/43.  
 DR N-PSDB; AAT90565.  
 DR  
 XX  
 XX Preventing apoptosis by blocking binding of interleukin-1beta to its  
 PT receptor - useful for, e.g. treating tumours, and inhibiting  
 PT oncogenic transformation  
 PS Example 5; Fig 7; 42pp; English.  
 XX  
 XX This is a cell death protein ICH-11. The cell death caused by this  
 CC ICH-11 can be prevented by a new method using IL-1 receptor antagonist  
 CC (IL-1Ra). IL-1Ra is also used in a method for preventing programmed cell  
 CC death by blocking the binding of interleukin-1 beta (IL-1 beta) to its  
 CC receptor. Other methods for modulating programmed cell death are provided  
 CC in the specification like a method of modulating apoptosis by activating  
 CC the IL-1 beta converting enzyme (ICE) pathway and IL-1 beta production,  
 CC a method for altering levels of hypoxia-induced cell death by blocking  
 CC IL-1-mediated signal transduction, a method for killing oncogenically  
 CC transformed cells by stimulating apoptosis with IL-1 beta or tumour  
 CC necrosis factor alpha (TNF alpha), a method of inhibiting hypoxia-induced  
 CC cell death by transfecting cells with the CrmA gene (of cowpox), and a  
 CC method for modulating apoptosis by downregulating the IL-1 receptor.  
 CC IL-1Ra inhibits apoptosis induced by trophic factor depletion or hypoxia,  
 CC while mature IL-1 beta induces cell death through a pathway independent  
 CC of CrmA-sensitive gene activity, and cooperates with ICE and ICH-11 in  
 CC apoptosis. Pro-IL-1 beta is the first substrate of any apoptosis-inducing  
 CC gene. Increasing/decreasing cells death can be used for the treatment of  
 CC tumours (or other conditions where apoptosis is involved). Altering cell  
 CC death can also be used for inhibiting oncogenic transformation, and to  
 CC treat complications involving apoptosis in cases of hypoxia or ischaemia.  
 CC The methods can also be used to screen for agents that modulate  
 CC apoptosis. When IL-1 beta is produced endogenously (via ICE) it mediates  
 CC cell death, but when added exogenously it may stimulate death if it binds  
 CC to its receptor after application of apoptotic stimulus or inhibit it by  
 CC binding to the receptor before application of the stimulus.  
 CC  
 SQ Sequence 435 AA;  
 XX  
 XX Query Match 23.3%; Score 289; DB 18; Length 435;  
 Best Local Similarity 31.1%; Pred. No. 1.4e-21;  
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;  
 QY 29 REGSEEDLDALEHMFROLFESTMKRDPATQFOELEKFOQADISREDPVSCAFVILMA 88  
 DB 202 RSGGDVHSTLVTLFKLGVGVHVLCDQTADQEMQKLNFAQ-LPAHVTSDC-IVALLS 259  
 QY 89 HGRGFLKGEDEVKLENLEALNNKQCALRAKPVYIIQACRGQRDPG----- 140  
 DB 260 HGVEGATYGVNDGKLQLEVFQLEFDNANCPSLQNKPMFIOACRGDETRDGVQDQDGN 319  
 QY 141 -----ETVGSDEIVWIKDSPTPTPTDYLHVSTVEGYIAYRHDOGSCFIOTLV 192  
 DB 320 HAGSPGCEESDAGE-----KLPRKRLPTRSDMTCGYACLGTAAMNTKSGSWIIEALA 374  
 QY 193 DVFTKR--KGHILELLEVTTRMAEALVOEGKAKTN-----PEIOTLRLKRLYL 241  
 DB 375 QVFSERACDMHIVADMLVKNALIKD---REGVAPGTFFHRCKEMSEYCSITLCHRLYL 428  
 Search completed: February 26, 2003, 12:19:03  
 Job time : 31.8526 secs

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GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: February 26, 2003, 12:17:35 ; Search time 28.4861 Seconds  
(without alignments)  
877.445 Million cell updates/sec

Title: US-09-989-903-2

Perfect score: 1350

Sequence: 1 KPMESEMSDPOPLQEEYD.....KPRKNPEVQSTLRKLYIQ 260

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	940.5	69.7	242	2 JC7517	caspase-14/a - hum
2	281	20.8	277	2 JC5410	CPP32 protein - mo
3	274.5	20.3	435	2 A54821	apoptosis regulato
4	274.5	20.3	452	2 JC6507	caspase-2 - rat
5	273	20.2	277	2 A55315	cysteine proteinas
6	268	19.9	454	2 JC7123	caspase-9 long cha
7	265	19.6	277	2 SC64710	cysteine proteinas
8	255.5	18.9	212	2 I67437	cysteine proteinas
9	253	18.7	416	2 G02635	ICE-LAP6 - human
10	253	18.7	503	2 A49429	interleukin-1 beta
11	231.5	17.1	495	2 T20038	hypothetical prote
12	219	16.2	182	2 I67436	interleukin-1 beta
13	215.5	16.0	311	2 B56084	interleukin-1 beta
14	215.5	16.0	383	2 A56084	interleukin-1 beta
15	215.5	16.0	404	2 A42677	interleukin-1 beta
16	203	15.0	418	2 B57511	interleukin-1 beta
17	201.5	14.9	482	2 A46495	IL-1 beta converta
18	200	14.8	312	2 B54821	apoptosis regulato
19	190.5	14.1	377	2 A57511	interleukin-1 beta
20	188.5	14.0	263	2 C56084	interleukin-1 beta
21	186	13.8	826	2 T43638	caspase-related pr
22	156	11.6	536	2 T43633	hypothetical prote
23	154	11.4	488	2 T13385	hypothetical prote
24	147.5	10.9	642	2 T27021	interleukin-1 beta
25	142	10.5	136	2 I53300	nitric-oxide synth
26	102	7.6	1429	2 S16233	H+-transporting tw
27	99	7.3	505	2 S39520	hypothetical prote
28	97.5	7.2	819	2 T19351	amino acid ABC tra
29	96.5	7.1	248	2 C82376	

30	95.5	7.1	843	2 A47132	major vault protei
31	95.5	7.1	880	2 F75103	conserved hypochet
32	94.5	7.0	1095	2 PC1114	SKC225 protein -
33	94	7.0	617	2 D96978	hypothetical prote
34	94	7.0	1875	2 S38173	myosin-like protei
35	93.5	6.9	747	2 D95862	probable sensor ha
36	93	6.9	544	2 A42464	microbial metallo
37	92.5	6.9	952	2 D86179	hypothetical prote
38	92.5	6.9	1093	2 A31758	phosphorylase kina
39	92.5	6.9	1093	2 A31758	phosphorylase kina
40	92.5	6.9	1156	2 B70356	chromosome assembl
41	92	6.8	700	2 E69146	sensory transducti
42	91.5	6.8	469	2 S17813	circ protein - Rho
43	91.5	6.8	1920	2 A53188	perlecanin - mous
44	91.5	6.8	2670	2 A46719	inositol 1,4,5-tri
45	91	6.7	971	2 A70179	exodeoxyribonuclea

## ALIGNMENTS

## RESULT 1

JC7517 caspase-14/a - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C:Accession: JC7517

R:Reckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A:Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte

A:Reference number: JC7517; MUID:20517231; PMID:11062009

A:Contents: Epidermal keratinocytes

A:Accession: JC7517

A:Molecule type: mRNA

A:Residues: 1-242 <ECK>

C:Cross-references: GB:AF097874

C:Comment: This enzyme accumulates during keratinocyte differentiation and is activated

C:Gene(s):

A:Gene: casp-14/a

A:Map position: 19p13.1

A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C:Keywords: differentiation

Query Match 69.7%; Score 940.5; DB 2; Length 242;  
Best Local Similarity 71.3%; Pred. No. 2, ie-63;  
Matches 181; Conservative 31; Mismatches 29; Indels 13; Gaps 2;

QY	8	MSDPQLQEEHYDMSGARLALTLCTKARGSEVDMELRMFRLKFEETMKRDPPTAQ	67
DB	1	MSNRSLEEEKYDMSGARLALTLCTKARGSEEDLDALHMFRLKFEETMKRDPPTAQ	60
QY	68	FLERLDFEFTIDNMEPVSQAFVLMAGBEGILLKEDEKMRVLEDFEVLNNKCAL	127
DB	61	FOELERFOALISREDPVSCAFVLMAGREGFLKEDEKMRVLEDFEVLNNKCAL	120
QY	128	RGRKVVIIQACGEHDPPEELRGNEELGDEELGDE-VAVYKNNPQSPPTDTHI	186
DB	121	RARKVVIQACRGEQDPG-----ETVGDEELVAVYKSPQPTPTDTHV	168
QY	187	YSTVEGLSYRHEKSGFIQTLTDFEIHKKGSLLEETETRLMANTVEQSEKPRKV	246
DB	169	YSTVEGLIAYRHQKSGFIQTLTDFEIVTKRKHLELTETRMALALVQSEKARKTN	228
QY	247	PEVQSTLRKLYIQ 260	
DB	229	PEIQSTLRKRLYIQ 242	

## RESULT 2

JC5410 CPP32 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 17-Mar-1999

C/Accession: J05410  
 R/Mkaseg, T.; Uraae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.  
 Biochem. Biophys. Res. Commun. 231, 770-774, 1997  
 A/Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activation  
 A/Reference number: J05410; MUID:97224429; PMID:9070890  
 A/Accession: J05410  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-277 <MUR>  
 A/Cross-references: DDBJ:D86352  
 A/Experimental source: embryo  
 C/Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 20.8%; Score 281; DB 2; Length 277;  
 Best Local Similarity 30.8%; Pred. No. 7.5e-14;  
 Matches 82; Conservative 45; Mismatches 91; Indels 48; Gaps 10;

Qy 16 EERYMSGARLALTLCTV-----KARGSEVDMEALERMFRYKFEETMKRDPTA 65  
 Db 34 DSSYKMDPEMIGICITITKNFKHKGSTGMSRSGTVDANLRETFMGLKYEVNKNKDLTR 93  
 Qy 66 QQFLELDEFQOTIDNWEPPVSCAFV-VLMAGEGLKGBEKNVRLEDLEFVANNKC 124  
 Db 94 ERMELMD---SVSKEDHSKRSFVCVLLSHGDEGVIFGTNGP-VDLKRLTSFRRGDYC 148  
 Qy 125 KALRQPKPVYIIQACRGEHRDPGEELRGNEELGDEBELGDEVAVLKNNPQSIPTYDTL 184  
 Db 149 RSLTKPKPLFIQACRGTELDGCIETDSTGBEMA-----CQKLPVEADPL 194  
 Qy 185 HIYSTEGLSYRHDEKSGFIQTITD--VFHKKGSILEETRIEMANTEVMOEQK 241  
 Db 195 YAVSTAPGVYWRNKSQSGWFIQSLCSMKLYAHK---LEFMHILTRV--NRKVATEPE 248  
 Qy 242 -----PRKVNPEVOSTLRKKLY 258  
 Db 249 SFSLDSTPHAKQIPCIIVSMLTRELY 274

## RESULT 3

A54821  
 Apoptosis regulator ICH-1, stimulatory form L - human  
 C/Species: Homo sapiens (man)  
 C/Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
 C/Accession: A54821  
 R/Mang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.  
 Cell 78, 739-750, 1994  
 A/Title: ICH-1, an Ice/ced-3-related gene, encodes both positive and negative regulators  
 A/Reference number: A54821; MUID:94373811; PMID:8087842  
 A/Accession: A54821  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-435 <MAN>  
 A/Cross-references: GB:U13021; NID:9537291; PID:9537292  
 C/Keywords: alternative splicing; apoptosis

Query Match 20.3%; Score 274.5; DB 2; Length 435;  
 Best Local Similarity 29.7%; Pred. No. 4e-13;  
 Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;

Qy 36 REGSEVDMEALERMFRYKFEETMKRDPTAQOFLBELDEFQOTIDNWEPPVSCAFVIMA 95  
 Db 202 RSGGVDDHTLVTLFRLGVDVHVLCDQQAQEMQEKLNFAQ-LPAHRTDSC-IVALIS 259  
 Qy 96 HGEELKGEDEKVRLEDLEFVANNKNCALRGKPVYIIQACRGEHRDPGEELRGNEE 155  
 Db 260 HGVEGAIYGVDDKLTQLQLEVEFLPDNANCPSLQNKPKMFFIQACRGDETDGVDQDQGN 319  
 Qy 156 LGGDEBELGDEVAVLKNNPQSIPTYDTLHIYSTEGLSYRHDEKSGFIQTITDVFH 215  
 Db 320 HAQSGCESDQKELPKMRLEPTSDMTCGACLCGTAMRTKSGSYIEHLAQVSE 379  
 Qy 216 KKGS--ILELTEITRLMANTEVMOEGRP---RKVNPEVOSTLRKKLY 259

Db 380 RACDMHVAIDLKVNVALIKREGVAPGTEFHRCKEMSEYCSLGRHLYL 428

## RESULT 4

J06507  
 caspase-2 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
 C/Accession: J06507  
 R/Sato, N.; Morigan, C.E.; Uchiyama, Y.; Oppenheim, R.W.  
 Gene 202, 127-132, 1997  
 A/Title: Cloning and expression of the cDNA encoding rat caspase-2.  
 A/Reference number: J06507; MUID:98087427; PMID:9427555  
 A/Accession: J06507  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-452 <SAT>  
 A/Cross-references: GB:U77933; NID:92769705; PIDN:AA96379.1; PID:92769706

Query Match 20.3%; Score 274.5; DB 2; Length 452;  
 Best Local Similarity 30.6%; Pred. No. 4.2e-13;  
 Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

Qy 36 REGSEVDMEALERMFRYKFEETMKRDPTAQOFLBELDEFQOTIDNWEPPVSCAFVIMA 95  
 Db 219 RSGGVDDHTLVTLFRLGVDVHVLCDQQAQEMQEKLNFAQ-LPAHRTDSC-IVALIS 276  
 Qy 96 HGEELKGEDEKVRLEDLEFVANNKNCALRGKPVYIIQACRGEHRDPG---EELRG 152  
 Db 277 HGVEGAIYGVDDKLTQLQLEVEFLPDNANCPSLQNKPKMFFIQACRGDETDGVDQDQGN 336  
 Qy 153 NEELGDEBELGDEVAVLKNNPQSIPTYDTLHIYSTEGLSYRHDEKSGFIQTITDV 212  
 Db 337 HAQSGCESDQKELMK---MRLEPTSDMTCGACLCGTAMRTKSGSYIEHLAQV 393  
 Qy 213 FHKKS--ILELTEITRLMANTEVMOEGRP---RKVNPEVOSTLRKKLY 259  
 Db 394 FSRACDMHVAIDLKVNVALIKREGVAPGTEFHRCKEMSEYCSLGRHLYL 445

## RESULT 5

A55315  
 cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human  
 N/Alternate names: cysteine proteinase CPP32  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 01-Dec-2000  
 C/Accession: A55315; S58899; I39005  
 R/Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.  
 J. Biol. Chem. 269, 30761-30764, 1994  
 A/Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans  
 A/Reference number: A55315; MUID:95074098; PMID:7983002  
 A/Accession: A55315  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-277 <FER>  
 A/Cross-references: GB:U13737; NID:9561665; PIDN:AA65015.1; PID:9561666  
 R/Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.; Yu, V.L.; Miller, D.K.  
 Nature 376, 37-43, 1995  
 A/Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian  
 A/Reference number: S58899; MUID:95319529; PMID:7596430  
 A/Accession: S58899  
 A/Molecule type: protein  
 A/Residues: 29-46;176-189, 'E',191-193 <NIG>  
 R/Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier, Cell 81, 801-809, 1995  
 A/Title: Yama/ CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease  
 A/Reference number: A56924; MUID:95292347; PMID:7774019  
 A/Accession: I39005  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-189, 'E',191-277 <RES>  
 A/Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569



C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 20.2%; Score 273; DB 2; Length 277;

Best Local Similarity 31.5%; Pred. No. 3e-13; Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

```

Qy 6 SEMSDPPLQEEERYDMSGARLALTLCTVCT-----AREGSEVDMALERNFRYLK 55
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 SESWDGSLDINSYKMDYPEMGDLCTIINNKNFKHSTGNTSGTDVDANLRETFRNLYK 83
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 56 ESTMKRPTAQQFLBELDEFQOTIDNWEPEVSCAFV-VLMAHGEGLKGEDEKVRLED 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 EVRNKNDLTLR-----EEIVELMRDVSKEDEHSKRSFVCLLSHGEGEIIFGTNGP-VDLKK 138
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 115 LFEVLNKNCKALRGKPKVYIIQACRGEHRDPGEELRGNEELSGDEEVLKNNP 174
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 ITNFRGDRCSLTGKPKFLFIIOACRGTELDGIE---TDSGDV---DDMKCHK--- 186
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 175 QSIPTVDTLHIYSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILELTEITRLMANT 234
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 --IVDADFLVASTAPGYSGWRNSKDGSWFIQSLC-AMLKQYADKLEFMIHLTRV--NR 241
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 235 EYVMEGK-----PRKNPEVOSTLRKLY 258
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 242 KVATEPESFSDATFPAKKQIPCIIVSMILTKELY 274
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

#### RESULT 6

caaspase-9 long chain - mouse  
C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: J07123

R;Pujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.  
Biochem. Biophys. Res. Commun. 264, 550-555, 1999

A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.

A;Reference number: J07123; MUID:20001956; PMID:10529400

A;Accession: J07123

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-454 <FU>

A;Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 19.9%; Score 268; DB 2; Length 454;

Best Local Similarity 30.2%; Pred. No. 1.3e-12; Matches 74; Conservative 45; Mismatches 96; Indels 30; Gaps 8;

```

Qy 36 REGSEVDMALERNFRYLKPESTMKRDPPTAQQFLBELDEFQOTIDNWEPEVSCAFV 95
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 218 RTGSNIDRDKLEHRPMLRFVWEVNDLTAKKMTALMEMAH---RNHRALDCFVVILS 274
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 96 HGEE-----GLKGEDEKVRLEDLFEVLNKNCKALRGKPKYIIQACRGEHRDGE 148
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 275 HGCQASHLQFPGAVYGTGDCSVSIEKIVINFGSGCPSLGKPKFLFIQACGGECKHGF 334
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 149 ELRGNEELG---GDEELGDEVAVLKNPQ-----SIPVYDTLHIYSTVEGYLS 195
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 335 EVACTSSGGRLLDSDSE---PDATPFGCEPRRLDGLDAVSSILPTSDILVYSTFPGVVS 391
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 196 YRHDEKSGSFIQTLTDVFIHKKSILELTEITRLMANTVEWQGEKPRKNPEVOSTLRK 255
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 392 WRDKSGSFWIETLDGILFQWARS--EDLQSLLRVANA-VSEKTYKQI-PGCNPLRK 447
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 256 KLYVQ 260
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 448 KLFKK 452
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

#### RESULT 7

S64710  
cysteine proteinase (EC 3.4.22.-) CP32 - Chinese hamster

C;Species: Cricetus griseus (Chinese hamster)

C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999

C;Accession: S64710; S72395

R;Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.

EMBO J. 15, 1012-1020, 1996

A;Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CP32 during

A;Reference number: S64710; MUID:96183185; PMID:8605870

A;Accession: S64710

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-277 <MAN>

A;Cross-references: EMBL:U27463

R;Wang, X.

submitted to the EMBL Data Library, May 1995

A;Reference number: S72395

A;Accession: S72395

A;Molecule type: mRNA

A;Residues: 1-79, 'A', '81-146, 'Y', '148-277 <MAN>

A;Cross-references: EMBL:U27463; NID:91244443; PIDN:AB01511.1; PID:91244444

C;Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 19.6%; Score 265; DB 2; Length 277;

Best Local Similarity 33.1%; Pred. No. 1.2e-12; Matches 78; Conservative 35; Mismatches 85; Indels 38; Gaps 9;

```

Qy 36 REGSEVDMALERNFRYLKPESTMKRDPPTAQQFLBELDEFQOTIDNWEPEVSCAFV-VLM 94
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 RSGTDVDAKLRERFMNLKYEVRKNDLTLR-----EEIVELMKNASKEDHSKRSFVCL 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 95 AHGEGGLKGEDEKVRLEDLFEVLNKNCKALRGKPKVYIIQACRGEHRDPGEELRGNE 154
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 SHGDEGVIFGTGDP-IDLKULTSYFRGDRCSLTGKPKFLFIQACRGTELDGIE--TDSGT 178
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 155 ELGDEELGDEVAVLKNPQSIPTVDTLHIYSTVEGYLSYRDEKSGSFIQTLTDVFIHK 211
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 E-----DDMKC-----QKIPVADFLVASTAPGYSGWRNSKDGSWFIQSLCMLK 224
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 212 VFHKKSILELTEITRLMANTVEWQGEK-----PRKNPEVOSTLRKLY 258
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 225 LVAKH---LEFMHILTRV--NRKVATEPESFSDATFPAKKQIPCIIVSMILTKELY 274
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

#### RESULT 8

167437

cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I67437

R;Flaws, J.A.; Kugu, K.; Tbovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfeld, A.N.; Tilly

Endocrinology 136, 5042-5053, 1995

A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cell

nulosa cells of the ovarian follicle.

A;Reference number: I53300; MUID:96042508; PMID:7588240

A;Accession: I67437

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-212 <RES>

A;Cross-references: EMBL:U34685; NID:91004370; PIDN:AAC52261.1; PID:91004371

C;Keywords: cysteine proteinase; hydrolase

Query Match 18.9%; Score 255.5; DB 2; Length 212;

Best Local Similarity 31.4%; Pred. No. 4.4e-12; Matches 72; Conservative 38; Mismatches 82; Indels 37; Gaps 9;

```

Qy 16 EERYDMSGARLALTLCTV-----KAREGSEVDMALERNFRYLKPESTMKRDPPTA 65
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 DSSYKMDYPEMGDLCTIINNKNFKHSTGMSANGTVDVDANLRETFMALKEVRKNDLTLR 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 66 QQFLBELDEFQOTIDNWEPEVSCAFV-VLMAHGEGLKGEDEKVRLEDLFEVLNKNCK 124
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 EIMELND-----SVSKPDHGRSSFCVILSHGDEGVIFGTNGP-VDLKKLTSFPRDGYC 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 125 KALRGKPKVYIIQACRGEHRDPGEELRGNEELGDEBELGDEVAVLKNPQSIPTVYDTL 184
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 RSLTGKPKFLFIQACRGTELDGIE---TDSGDV-----DVVACQK-----VVEADFL 165
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Oy 185 HIYSTEVEGLSYRHEDEKSGFIQTL---TDVFHKKGSIILETEITRL 230  
 Db 166 YAYSSAPGYISWRNSRGSGSWFIQSLCAMLKYAHK---LEPMHILITRY 210

## RESULT 9

ICE-LAP6 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 05-Nov-1999  
 C:Accession: G02635  
 R:Duan, H.; Oryh, K.; Chinaiyan, A.M.; Poixler, G.G.; Froelich, C.J.; He, W.W.; Dixit, submitted to the EMBL Data Library, April 1996  
 A:Reference number: H01513  
 A:Accession: G02635  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <DNA>  
 A:Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAG50640.1; PID:g1336027

Query Match 18.7%; Score 253; DB 2; Length 416;  
 Best Local Similarity 29.1%; Pred. No. 1,6e-11;  
 Matches 74; Conservative 47; Mismatches 89; Indels 44; Gaps 8;

Oy 34 KAREGEVDMELERMFRLKFEFTMKRDPDPTAQOFLBELDEFOQITIDWEEPVSCAFVVL 93  
 Db 178 RTRTSNIDCELRFRFSSLHFMVEKGDLTAKKVALLELARQDHG---ALDCCVYI 234  
 Oy 94 MAHGE-----GLLKGEDEKVRLEDFEVLNKNCALRGKPKVYIIQACRGEHRDP 146  
 Db 225 LSHGQASHLQPGAVYGTGDCPVSVETKVINFGTSCSLGKPKLFTIQCGEGQKH 294  
 Oy 147 GELRGNEELGDEELGDEVAVALKKNPQ-----SITTYDTLHI 186  
 Db 295 GEEVASTSP--EDESPQ-----SNPEPDATPQEGRTFDODAISLPTPSDIFVS 344  
 Oy 187 YSTVGYSYRHEDEKSGFIQTLTDVFIHKKGSIILETEITRLMANTEVEGKPRKVN 246  
 Db 345 YSTFGFYSWRNSRGSGSWFIQSLCAMLKYAHK---LEPMHILITRY 210  
 Oy 247 PEVOSTLRKLYLQ 260  
 Db 401 PGCFFFLRKLFFK 414

## RESULT 10

A49429  
 Interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-2000  
 C:Accession: A49429; T37312  
 R:Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.  
 Cell 75, 641-652, 1993

A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int  
 A:Reference number: A49429; MUID:94061982; PMID:8242740  
 A:Accession: A49429  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-503 <YUA>  
 A:Cross-references: GB:L29052; NID:96503232; PIDN:AAA27982.2; PID:96503233

A:Note: sequence extracted from NCBI backbone (NCBI:139825, NCBI:139826)  
 A:Accession: T37312

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-417, 'R', 'A', '419-503 <YU2>

A:Cross-references: EMBL:L29052; PIDN:AAA27982.1

A:Gene: ced-3  
 A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 18.7%; Score 253; DB 2; Length 503;  
 Best Local Similarity 28.9%; Pred. No. 2e-11;

Matches 69; Conservative 49; Mismatches 101; Indels 20; Gaps 7;

Oy 36 REGSEVDMELERMFRLKFEFTMKRDPDPTAQOFLBELDEFOQITIDWEEPVSCAFVYLA 95  
 Db 259 RRGTRADKNDLTLNLFRCMGYIVICKNDLTGRGMLTTRDFAK---HSHGDSALIVLS 314  
 Oy 96 HGEGLLKGEDEKVRLEDFEVLNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEE 155  
 Db 315 HGEENVIIQVDDIPISHEIYDLNLAANAPRLANKPKIVFQACRGERRDGPFVLSVD 374  
 Oy 156 -----LGGSEELG--DEVAVALKKNPQST---PYTDTLHIYSTVEGLSYRHEKG 202  
 Db 375 GVPAFLRGMWNRDGPLNFNGCVRPVQVQWRKKPQADLLIYATTAQVSWRNSARG 434  
 Oy 203 SGFIQTLTDVF-IHKKG-SIILETEITRLMA-NTEVWQEGKPKVNPVOSTLRKLY 258  
 Db 435 SWFIQAVCEVSTAKMDVVELLTVNKKVACFGISQSGNIIKQPEMTSRLLKIFY 493

## RESULT 11

hypothetical protein C48D1.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T20038  
 R:Burton, J.  
 submitted to the EMBL Data Library, October 1996

A:Reference number: Z19214  
 A:Accession: T20038  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-495 <WLL>

A:Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2  
 A:Experimental source: clone C48D1

A:Gene: CESP:C48D1.2

A:Map position: 4

A:Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 17.1%; Score 231.5; DB 2; Length 495;  
 Best Local Similarity 28.3%; Pred. No. 8e-10;  
 Matches 60; Conservative 47; Mismatches 86; Indels 19; Gaps 6;

Oy 36 REGSEVDMELERMFRLKFEFTMKRDPDPTAQOFLBELDEFOQITIDWEEPVSCAFVYLA 95  
 Db 258 RRGTRADKNDLTLNLFRCMGYIVICKNDLTGRGMLTTRDFAK---HSHGDSALIVLS 313  
 Oy 96 HGEGLLKGEDEKVRLEDFEVLNKNCALRGKPKVYIIQACRGEHRDPGEELRGNEE 155  
 Db 314 HGEENVIIQVDDIPISHEIYDLNLAANAPRLANKPKIVFQACRGERRDGPFVLSVD 373  
 Oy 156 -----LGGSEELG--DEVAVALKKNPQST---PYTDTLHIYSTVEGLSYRHEKG 202  
 Db 374 GVPAFLRGMWNRDGPLNFNGCVRPVQVQWRKKPQADLLIYATTAQVSWRNSARG 433  
 Oy 203 SGFIQTLTDVF-IHKKG-SIILETEITRLMA 232  
 Db 434 SWFIQAVCEVSTAKMDVVELLTVNKKVYA 465

## RESULT 12

I67436  
 Interleukin-1 beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I67436

R:Flaws, J.A.; Kugu, K.; Tripovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tilly, submitted to the EMBL Data Library, April 1996

A:Title: Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cel  
 nuloa cells of the ovarian follicle.

A:Reference number: I53300; MUID:96042508; PMID:7588240  
 A:Accession: I67436  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-182 <RES>  
 A:Cross-references: EMBL:U34684; NID:g1004368; PIDN:AAC52260.1; PID:g1004369

Query Match 16.0%; Score 219; DB 2; Length 182;  
 Best Local Similarity 32.1%; Pred. No. 2e-09;  
 Matches 51; Conservative 39; Mismatches 61; Indels 8; Gaps 4;

Qy 36 REGSEVDMELERMFRYLKESTKKRDPDPTAQOFLBEDEFQOTIDNMEBPVSCAFVILMA 95  
 Db 22 RSGGDVHTLVTLVFLKLGYNVHLVDYDTAQEMQEKQNFQQLPAHVDSCL-IVALLS 79  
 Qy 96 HGEGLIKGEDEKKNVLEDFEVLNKNCKALRGKPKVYIIQACRGHRDPC--EELRG 152  
 Db 80 HGVGGGIVGVGDKLQLQGVFRLFDNANCSLQNKPKMFIIQACRGDETRGVVQDQGN 139

Qy 153 NEELGDEELGDEVAVLKNKPPISPTVTDLHLYSTVE 191  
 Db 140 HAOPGCESDTVKEELMK--MRLPTRSDMTCVYACLK 175

# RESULT 13

interleukin-1beta converting enzyme gamma isozyyme - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 05-Nov-1999  
 C:Accession: B56084  
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.  
 J. Biol. Chem. 270, 4312-4317, 1995  
 A:Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver

A:Reference number: A56084; MUID:95181414; PMID:7876192  
 A:Accession: B56084  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-311 <ALN>  
 A:Cross-references: GB:U13698; NID:g717041; PIDN:AAC50108.1; PID:g717042

C:Gene: IL1BCE  
 C:Genetics:  
 A:Keywords: alternative splicing

Query Match 16.0%; Score 215.5; DB 2; Length 311;  
 Best Local Similarity 30.3%; Pred. No. 7.1e-09;  
 Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

Qy 22 SGARLALTLCVTK-----AREGSEVDMELERMFRYLKESTKKRDPDPTAQOFLBEDEF- 75  
 Db 67 SRRRLALICNEERFDSIPRTGAEVDITGTMMLQNLGVSVDKKNLTASDMTELEAFA 126  
 Qy 76 ----QOTIDNMEBPVSCAFVILMAHG-EEGLL-KGEDEK--MVRLEDLFEVLNKNCKA 126  
 Db 127 HRPEHKTSDS-----TFLVFMHSHGIRREGICGKKSSEQVPDILQNALIFNMLNTKNCPS 179  
 Qy 127 LRGPVKYIIQACRGHRDPC-----EELRGNEELGDEELGDEVAVLKNKPPISPT 179  
 Db 180 LKQPKYIIQACRGD--SPGVWFKDSVSGNLSPTTEFEEDD--AIKKAHIEK--- 232  
 Qy 180 YTDLHLYSTVEGLSVRHEKSGFIQTLTDVFIHKKSILLL-TEETRLMANTEVMQ 238  
 Db 233 --DFIACSSPTPDVNSVRHPTMGVSFIGRLIE--HMQEVACSCDVEIFRKVRFSEOP 287  
 Qy 239 EGKPRKVNPEVOSTLRKLYL 259  
 Db 288 DGRAQMPTE-RVTLTRCFYL 307

# RESULT 14

interleukin-1beta converting enzyme beta isozyyme - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 05-Nov-1999  
 C:Accession: A56084  
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.  
 J. Biol. Chem. 270, 4312-4317, 1995

A:Title: Cloning and expression of four novel isoforms of human interleukin-1beta convert

A:Reference number: A56084; MUID:95181414; PMID:7876192  
 A:Accession: A56084  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-383 <ALN>  
 A:Cross-references: GB:U13697; NID:g717039; PIDN:AAC50107.1; PID:g717040

C:Gene: IL1BCE  
 C:Genetics:  
 A:Keywords: alternative splicing

Query Match 16.0%; Score 215.5; DB 2; Length 383;  
 Best Local Similarity 30.3%; Pred. No. 9.2e-09;  
 Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

Qy 22 SGARLALTLCVTK-----AREGSEVDMELERMFRYLKESTKKRDPDPTAQOFLBEDEF- 75  
 Db 139 SRRRLALICNEERFDSIPRTGAEVDITGTMMLQNLGVSVDKKNLTASDMTELEAFA 198

Qy 76 ----QOTIDNMEBPVSCAFVILMAHG-EEGLL-KGEDEK--MVRLEDLFEVLNKNCKA 126  
 Db 199 HRPEHKTSDS-----TFLVFMHSHGIRREGICGKKSSEQVPDILQNALIFNMLNTKNCPS 251

Qy 127 LRGPVKYIIQACRGHRDPC-----EELRGNEELGDEELGDEVAVLKNKPPISPT 179  
 Db 252 LKQPKYIIQACRGD--SPGVWFKDSVSGNLSPTTEFEEDD--AIKKAHIEK--- 304

Qy 180 YTDLHLYSTVEGLSVRHEKSGFIQTLTDVFIHKKSILLL-TEETRLMANTEVMQ 238  
 Db 305 --DFIACSSPTPDVNSVRHPTMGVSFIGRLIE--HMQEVACSCDVEIFRKVRFSEOP 359

Qy 239 EGKPRKVNPEVOSTLRKLYL 259  
 Db 360 DGRAQMPTE-RVTLTRCFYL 379

# RESULT 15

interleukin-1 beta converting enzyme (EC 3.4.22.-) - human

C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
 C:Accession: A54263; A42677; S21734; S24164  
 R:Gerrett, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A.  
 Science 256, 97-100, 1992  
 A:Title: Molecular cloning of the interleukin-1beta converting enzyme.  
 A:Reference number: A42677; MUID:92229430; PMID:1373520

A:Accession: A54263  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-404 <CE2>

A:Cross-references: GB:L27475  
 R:Gerrett, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T.A.  
 Science 256, 97-100, 1992  
 A:Title: Molecular cloning of the interleukin-1beta converting enzyme.

A:Reference number: A42677; MUID:92229430; PMID:1373520  
 A:Accession: A42677  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-404 <CE2>

A:Cross-references: GB:M87507; NID:g435598; PIDN:AAA66942.1; PID:g186286  
 R:Thorbertry, N.A.; Bull, H.G.; Calley, J.R.; Chapman, K.T.; Howard, A.D.; Kostura, M.  
 J.; Ding, G.J.F.; Egger, L.A.; Gaffney, E.P.; Limjoco, G.; Palyha, O.C.; Raju, S.M.; Rolé  
 cci, M.J.

Nature 356, 768-774, 1992  
 A:Title: A novel heterodimeric cysteine protease is required for interleukin-1beta proces

A:Reference number: S21734; MUID:92244318; PMID:1574116  
 A:Accession: S21734  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-404 <THO>  
 A:Cross-references: EMBL:X65019; NID:g33792; PIDN:CAA46153.1; PID:g33793  
 R:Kronheim, S.R.; Mumma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.; I  
 Arch. Biochem. Biophys. 296, 698-703, 1992

A:Title: Purification of interleukin-1beta converting enzyme, the protease that cleaves  
A:Reference number: S24164; MUID:92337439; PMID:1321594  
A:Accession: S24164  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 120-135, 'AX', 138-139, 'X', 141-142 <KRO>  
C:Genetics:  
A:Gene: GDB:IL1BC  
A:Cross-references: GDB:132368; OMIM:147678  
A:Map position: 11q23-11q23  
C:Keywords: cysteine protease; hydrolase

Query Match 16.0%; Score 215.5; DB 2; Length 404;  
Best Local Similarity 30.3%; Pred. No. 9.8e-09;  
Matches 79; Conservative 43; Mismatches 96; Indels 43; Gaps 13;

QY 22 SGARLALTLVTK-----ARSGSEVDMELERFRLKFEESTMKRDPPTAQOFLERLDEF- 75  
Db 160 SRTRLALILICNEEFPDSIPRRTGAEVDITGMTMLLQNLGYSVDKKNLTASDWTTELEAFA 219  
QY 76 ----QQTIDNNEEPVSCAFVVIIMAHG-EEGLL-KGEDEK--MVRLEDLFEVLNNKCKA 126  
Db 220 HRPEHKTSDS-----TFIVFMSHGIRREGICGKXSEQVPDILQNLAIENMLNTKNCPS 272  
QY 127 LRGRKRVYIIQACRGEHRDPG-----EELRNEBELGGDEELGGDEAVAILKNNPQSIPT 179  
Db 273 LKDRKRVIIIIQCRGD--SPGVWPFKDSVGSVGNLSLPTTEFEEDD--AIKKAHIEK--- 325  
QY 180 YTDTHITSTVSGYLSYRDEKSGSFIQTLDVFIHKKSIIEL--TEETRLMANTVWQ 238  
Db 326 --DFIAFCSSTPDNVSWRPTNGSVFIGRLIE--HMOEYACSDVEELFRKVRPSPEQP 380  
QY 239 EGKPRKVNPEVOSTLRKKLYL 259  
Db 381 DGRAGMPTE-RVTLTRCFYL 400

Search completed: February 26, 2003, 12:21:30  
Job time : 30.4861 secs

GenCore version 5.1.3  
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OM protein - protein search, using SW model

Run on: February 26, 2003, 12:14:00 ; Search time 8.80478 Seconds

(without alignments)  
1224.772 Million cell updates/sec

Title: US-09-989-903-2

Sequence: 1 KPDMSEMSDPQLQERVD.....KPRKNPEVQSTLRKLYIQ 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	1332	98.7	257	1	ICB2_MOUSE
2	940.5	69.7	242	1	ICB2_MOUSE
3	290.5	21.5	424	1	ICB2_MOUSE
4	276.5	20.5	435	1	ICB2_MOUSE
5	276	20.4	277	1	ICB2_MOUSE
6	274.5	20.3	435	1	ICB2_MOUSE
7	274	20.3	277	1	ICB2_MOUSE
8	273	20.2	277	1	ICB2_MOUSE
9	263	19.5	277	1	ICB2_MOUSE
10	259.5	19.2	496	1	ICB2_MOUSE
11	255.5	18.9	303	1	ICB2_MOUSE
12	254.5	18.9	303	1	ICB2_MOUSE
13	253	18.7	503	1	ICB2_MOUSE
14	250	18.5	416	1	ICB2_MOUSE
15	249.5	18.5	303	1	ICB2_MOUSE
16	249.5	18.5	382	1	ICB2_MOUSE
17	243	18.0	339	1	ICB2_MOUSE
18	235	17.4	276	1	ICB2_MOUSE
19	232.5	17.2	293	1	ICB2_MOUSE
20	231.5	17.1	282	1	ICB2_MOUSE
21	227.5	16.9	323	1	ICB2_MOUSE
22	226.5	16.8	299	1	ICB2_MOUSE
23	220	16.3	479	1	ICB2_MOUSE
24	219	16.2	312	1	ICB2_MOUSE
25	217.5	16.1	386	1	ICB2_MOUSE
26	215.5	16.0	404	1	ICB2_MOUSE
27	213	15.8	410	1	ICB2_MOUSE
28	211	15.6	404	1	ICB2_MOUSE
29	205	15.2	402	1	ICB2_MOUSE
30	203	15.0	418	1	ICB2_MOUSE
31	201.5	14.9	402	1	ICB2_MOUSE
32	200.5	14.9	405	1	ICB2_MOUSE
33	198.5	14.7	404	1	ICB2_MOUSE

34	198	14.7	521	1	ICB2_MOUSE
35	196.5	14.6	419	1	ICB2_MOUSE
36	190.5	14.1	377	1	ICB2_MOUSE
37	188.5	14.0	373	1	ICB2_MOUSE
38	175	13.0	377	1	ICB2_MOUSE
39	112	8.3	484	1	ICB2_MOUSE
40	102	7.6	1429	1	ICB2_MOUSE
41	101.5	7.5	480	1	ICB2_MOUSE
42	99	7.3	505	1	ICB2_MOUSE
43	95.5	7.1	843	1	ICB2_MOUSE
44	95.5	7.1	880	1	ICB2_MOUSE
45	94.5	7.0	1095	1	ICB2_MOUSE

## ALIGNMENTS

RESULT 1  
ICB2\_MOUSE  
ID ICB2\_MOUSE STANDARD; PRT; 257 AA.  
AC 089094;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (MICE).  
GN CASP14.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=99040667; PubMed=9823333;  
RA Ahmed M., Srinivasula S.M., Hegde R., Muketash R.,  
RA Fernandes-Alnemri T., Alnemri E.S.,  
RT "Identification and characterization of murine caspase-14, a new  
RT member of the caspase family."  
RT Cancer Res. 58:5201-5205(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6; TISSUE=Embryo;  
RX MEDLINE=9922069; PubMed=10203698;  
RA Van de Craen M., Van Loo G., Pye S., Van Criekinge W.,  
RA Van den Brande I., Molemans F., Fiers W., Declercq W.,  
RA Vandebaele P.,  
RT "Identification of a new caspase homologue: caspase-14."  
RT Cell Death Differ. 5:838-846(1998).  
RN [3]  
RP CHARACTERIZATION AND MUTAGENESIS OF CYS-136.  
RX MEDLINE=9909076; PubMed=9792675;  
RA Hu S., Shipas S.J., Vincenz C., Salvesen G., Dixit V.M.,  
RT "Caspase-14 is a novel developmentally regulated protease."  
RT J. Biol. Chem. 273:29648-29653(1998).  
CC -1- FUNCTION: SEEMS TO BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME  
B APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL  
TRANSDUCER OF CELL DEATH. MAY PLAY A ROLE IN ONTOGENESIS AND SKIN  
PHYSIOLOGY.  
CC -1- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- TISSUE SPECIFICITY: EMBRYO, ADULT LIVER AND LESS IN ADULT BRAIN  
AND KIDNEY.  
CC -1- PPM: CLEAVAGE BY GRANZYME B. CASPASE-8 AND -10 GENERATES THE  
TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
PROTEASE.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL:	AJ032997;	AAC6364.1;	-
DR	EMBL:	AJ007750;	CAA07678.1;	-
DR	HSSP:	P29466;	1ICE.	
DR	MEROPS:	C14.018;	-	
DR	MGP:	MGI:1335092;	Casp14.	
DR	InterPro:	IPR002398;	ICE.	
DR	InterPro:	IPR002138;	ICE_p10.	
DR	InterPro:	IPR001309;	ICE_p20.	
DR	Pfam:	PF00655;	ICE_p10;	1.
DR	Pfam:	PF00656;	ICE_p20;	1.
DR	SMART:	SM00115;	CASC.	1
DR	PROSITE:	PS01121;	CASPASE_HIS;	FALSE_NEG.
DR	PROSITE:	PS01122;	CASPASE_CYS;	FALSE_NEG.
DR	PROSITE:	PS50207;	CASPASE_P10;	1.
DR	PROSITE:	PS50208;	CASPASE_P20;	1.
KW	Hydrolase; Thiol protease; Apoptosis; Zymogen.			
FT	PROPEP	1	7	POTENTIAL.
FT	CHAIN	8	?	CASPASE-14 SUBUNIT P18 (POTENTIAL).
FT	CHAIN	?	257	CASPASE-14 SUBUNIT P11 (POTENTIAL).
FT	ACT_SITE	93	93	BY SIMILARITY.
FT	ACT_SITE	136	136	BY SIMILARITY.
FT	MUTAGEN	136	136	C->A: DECREASE IN DEATH-INDUCING ACTIVITY.
SQ	SEQUENCE	257 AA;	29458 MW;	A228D86DFEA0EB84 CRC64;

Query Match	98.7%	Score 1332	DB 1	Length 257
Best Local Similarity	100.0%	Pred. NO. 4.6e-94		
Matches 257; Conservative	0;	Mismatches 0;	Indels 0	Gaps 0

Oy	4	MESEMSDDPOLOEEHYDMSGARLLTLCVTARAGSEVDMBALEMRFRYLKPFSTIMKRD	63
Db	1	MESEMSDDPOLOEEHYDMSGARLLTLCVTARAGSEVDMBALEMRFRYLKPFSTIMKRD	60
Oy	64	TAQOFLBELDEFQOTIDNMBEVPSCAFVYLLMAHGBEGLKGEDKMYRLBDLFEVILNKK	123
Db	61	TAQOFLBELDEFQOTIDNMBEVPSCAFVYLLMAHGBEGLKGEDKMYRLBDLFEVILNKK	120
Oy	124	CKALMGKPKVYIIQACRGREHDPGEELNGBELGDEELGDEVAVALVKNPNOSIPITYDT	183
Db	121	CKALMGKPKVYIIQACRGREHDPGEELNGBELGDEELGDEVAVALVKNPNOSIPITYDT	180
Oy	184	LHIYSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILLETBEITRLMANTEVMOECKPR	243
Db	181	LHIYSTVEGYLSYRDEKSGSFIQTLTDVFIHKKSILLETBEITRLMANTEVMOECKPR	240
Oy	244	KVNPVOSTLRKKLYLQ 260	
Db	241	KVNPVOSTLRKKLYLQ 257	

	RESULT 2
1	ICEE_HUMAN
2	
3	ID_ICEE_HUMAN STANDARD; PRT; 242 AA.
4	AC P31944; O95823; (Rel. 26, Created)
5	DT 01-JUL-1993 (Rel. 40, Last sequence update)
6	DT 16-OCT-2001 (Rel. 41, Last annotation update)
7	DT 15-JUN-2002 (Rel. 41, Last annotation update)
8	DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14),
9	CASP14.
10	GN Homo sapiens (Human).
11	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
12	OC Mammalia; Eupheria; Primates; Carnivora; Homnidae; Homo.
13	OX NCBI_TaxID=9606;
14	OX [1]
15	RP SEQUENCE FROM N.A.
16	RP TISSUE=Brain;
17	RA Poyet U.-L., Sriivasula S.M., Fernandes-Alnemri T., Alnemri E.S.,
18	RT "Identification and characterization of human caspase 14.";
19	RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
20	[2]

```

RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes; PubMed=1286667'.
RX MEDLINE=93162043; PubMed=1286667'.
RA Rasmussen H.H., Van Damme J., Puype M., Geeser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME B
CC APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL TRANSDUCER
CC OF CELL DEATH.
CC -1- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC -----
DR EMBL; AF097874; AAD16173.1; -.
DR HSSP; P29466; LICE.
DR Aarhus/Ghent-2DPAGE; 6109; IEF.
DR MEROPS; C14.018; -.
DR Genew; HGNC:1502; CASP14.
DR MIM; 605848; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PRO0376; ILIBENZYM.E.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS01121; CASPASE_HIS; FALSE NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE NEG.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Apoptosis; zymogen.
KW PROPEP
FT CHAIN 1 ?
FT CHAIN ? 146 CASPASE-14 SUBUNIT 1 (POTENTIAL).
FT ACT_SITE 147 242 CASPASE-14 SUBUNIT 2 (POTENTIAL).
FT ACT_SITE 89 89 BY SIMILARITY.
FT ACT_SITE 132 132 BY SIMILARITY.
SQ SEQUENCE 242 AA; 27679 MW; E539FB7EBDB08A2 CRC64;

```

Query Match	69.7%	Score 940.5;	DB 1;	Length 242;
Best Local Similarity	71.3%	Pred. No. 1.9e-64;		
Matches 181; Conservative	31;	Mismatches 29;	Indels 13;	Gaps 2;

[illegible]

RESULT 3  
 ICE2\_CHICK STANDARD: PRT; 424 AA.  
 AC 098943;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).  
 GN CASP2 OR ICH1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn; TISSUE=Ovarian granulosa;  
 RX MEDLINE=97368127; PubMed=9224894;  
 RA Johnson A.L., Bridgham J.T., Bergeron L., Yuan J.;  
 RT "Characterization of the avian Ich-1 cDNA and expression of Ich-1L mRNA in the hen ovary";  
 RT Gene 192:227-233(1997).  
 RL  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER  
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING  
 CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOMERIS: ICH-1L (SHOWN HERE) AND ICH-1S;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-  
 CC TERMINI. ONLY THE ICH-1L FORM IS FOUND IN THE OVARY.  
 CC -1- PTM: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
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 CC EMBL; U64963; AAC29881.1; ALT\_INIT.  
 DR HSSP; P42574; ICP3.  
 DR MEROPS: C14.006.-;  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF006519; CARD; 1.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR PRINTS; PR00376; ILIBCNZYME.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PSS0209; CARD; 1.  
 DR PROSITE; PSS0123; CASPASE\_CYS; 1.  
 DR PROSITE; PSS0121; CASPASE\_HIS; 1.  
 DR PROSITE; PSS0207; CASPASE\_P10; 1.  
 DR PROSITE; PSS0208; CASPASE\_P20; 1.  
 KM Hydrolyase; Thiol protease; Zymogen; Alternative splicing.  
 FT PROPEP 1 140  
 FT CHAIN 141 308 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).  
 FT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).  
 FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).  
 FT DOMAIN 7 96 CARD.  
 FT ACT\_SITE 248 248 BY SIMILARITY.  
 FT ACT\_SITE 291 291 BY SIMILARITY.  
 FT VARSPIC 1 7 MISSING (IN ISOMER ICH-1S).  
 FT VARSPIC 294 424 DETROGDQDRGKGRNSPGCESDANKENKLRPTRS  
 FT DMLVKVNRQIKRGVAPGTEFRCKEMSEYCTLCRDLYL  
 FT FPGVVGPK -> GVSIGIHILPLPCCHCICCSMRGTGEMI

FT REMARK:GOIPQAVRVMQTRKXISSCVCLHAPI (IN  
 FT ISOFORM ICH-1S).  
 SO SEQUENCE 424 AA; 47959 MW; 792810508B8B2F60 CRC64;  
 Query Match 21.5%; Score 290.5; DB 1; Length 424;  
 Best Local Similarity 31.0%; Pred. No. 6.7e-15;  
 Matches 72; Conservative 53; Mismatches 94; Indels 13; Gaps 5;  
 QY 36 REGSEVDMALERFRYLKFEFTKRPDPTAOQFLSELDDEFQOTIDNMEEPSCAFVYLMA 95  
 DB 190 RSGGDVDCASLELLFKILGQVTFHQDSABEMBSALERSKLPDH--QDVDSCTVALLS 247  
 QY 96 HGEELKGEDEKXVRLLEDVFEVLNNKCALRGKPRVY11OACRGHRDPGEELRGNEE 155  
 DB 248 HGVEGVGYGTGKLLQGEAFRLFDNANCPNLQKPKMFFIOACRGDETRDGVDRDQKE 307  
 QY 156 LG--GDEELGDEVAVLKNPPOSIPPTDTLHYSVEGLSTRHEKSGFQTLTDV 212  
 DB 308 RSDSPGCEESDANKENLK--LRLPTRSDMICGVALCKGTAAARNTRKGSWYIEALTIV 364  
 QY 213 FTH--KKGSIETELTEITRLMANTEVMOEGKP--RYNPEVOSTLRKKLYL 259  
 DB 365 FAEDSDTHVADMLVKVNRQIKRGVAPGTEFRCKEMSEYCTLCRDLYL 416  
 RESULT 4  
 ICE2\_MOUSE STANDARD: PRT; 435 AA.  
 AC P29594; O08737;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2 protein).  
 GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=95047319; PubMed=7958843;  
 RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;  
 RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a  
 RT protein similar to the product of the Caenorhabditis elegans cell  
 RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";  
 RL Genes Dev. 8:1613-1626(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/An;  
 RX MEDLINE=97190206; PubMed=9038361;  
 RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,  
 RA van Loo G., Molemans F., Schotte P., van Cleyninge W., Beyaert R.,  
 RA Fiers W.;  
 RT "Characterization of seven murine caspase family members.";  
 RL FBS Lett. 403:61-69(1997).  
 RN [3]  
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=92328780; PubMed=1378265;  
 RA Kumar S., Tomooka Y., Noda M.;  
 RT "Identification of a set of genes with developmentally down-regulated  
 RT expression in the mouse brain.";  
 RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER  
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING  
 CC PROTEINS NECESSARY FOR CELL SURVIVAL. MAY BE IMPORTANT IN  
 CC MULTISTEP CARCINOGENESIS.  
 CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY  
 CC SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: HIGH LEVEL EXPRESSION SEEN IN THE EMBRYONIC

CNS, LIVER, LUNG, KIDNEY, SMALL INTESTINE, AND HAIR FOLLICLES OF  
VIBRISSAE. MODERATE EXPRESSION SEEN IN THE SKIN, ORAL MUCOSA,  
SKLETERAL MUSCLE, SUBMANDIBULAR GLAND AND THYMUS. IN THE ADULT, IT  
IS HIGHLY EXPRESSED IN SPLEEN, LUNG AND KIDNEY. MODERATELY IN THE  
BRAIN, HEART, TESTIS, LIVER. LOW LEVELS IN THE THYMUS, SKELETAL  
MUSCLE, OVARY AND GUT.  
-1- DEVELOPMENTAL STAGE: DURING EMBRYONIC DEVELOPMENT IS HIGHLY  
EXPRESSED IN SEVERAL TYPES OF MOUSE TISSUE UNDERGOING HIGH RATES  
OF PROGRAMMED CELL DEATH SUCH AS CENTRAL NERVOUS SYSTEM AND  
KIDNEY.  
-1- PIM: THE MATRE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT  
THAT OF OTHER CASPASES (BY SIMILARITY).  
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
-1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC  
CC EMBL: D28492; BAA25876.1; ALT\_INIT.  
CC EMBL: Y13085; CAA73527.1; ALT\_INIT.  
CC HSSP: P42574; 1CP3.  
CC MEROPS: C14.006; -.  
CC MGD: MGI:97295; Casp2.  
CC InterPro: IPR001315; CARD.  
CC InterPro: IPR002398; ICE.  
CC InterPro: IPR002138; ICE\_p10.  
CC InterPro: IPR001309; ICE\_p20.  
CC Pfam: PF00619; CARD; 1.  
CC Pfam: PF00655; ICE\_p10; 1.  
CC Pfam: PF00656; ICE\_p20; 1.  
CC PRINTS: PR00376; IL1BCENZYM.  
CC SMART: SMO0114; CARD; 1.  
CC SMART: SMO0115; CASc; 1.  
CC PROSITE: PS50209; CARD; 1.  
CC PROSITE: PS01122; CASPASE\_CYS; 1.  
CC PROSITE: PS01121; CASPASE\_HIS; 1.  
CC PROSITE: PS50207; CASPASE\_P10; 1.  
CC PROSITE: PS50208; CASPASE\_P20; 1.  
CC Hydrolase; Thiol protease; Apoptosis; Zymogen.  
CC PROPEP 1 152  
CC CHAIN 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).  
CC CHAIN 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).  
CC CHAIN 331 435 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).  
CC DOMAIN 15 103 CARD.  
CC ACT\_SITE 260 260 BY SIMILARITY.  
CC ACT\_SITE 303 303 BY SIMILARITY.  
CC MUTAGEN 303 303 C->G: LOSS OF FUNCTION.  
CC CONFLICT 71 71 MISSING (IN REF. 1).  
CC SEQUENCE 435 AA; 48896 MW; 898466A/6E7A676 CRC64;  
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Query Match 20.5%; Score 276.5; DB 1; Length 435;  
Best Local Similarity 30.6%; Pred. No. Re-14;  
Matches 71; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

Db 377 F5RACDWHVADMLVKVNALIKERGVAGTEFFHCKEMSEYCTLLCOQLYL 428  
RESULT 5  
ID ICE3 MOUSE STANDARD; PRT; 277 AA.  
AC P70677; O08668;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama  
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)  
DE (SCA-1) (LICE).  
OS CASP3 OR CPP32.  
GN Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358624; PubMed=8761296;  
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
RA Fletcher F.A.;  
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding  
RT a cysteine protease resembling interleukin-1 beta converting enzyme  
RT and CED-3.";  
RL Oncogene 13:749-755(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9724429; PubMed=9070890;  
RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;  
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and  
RT activation of CPP32 in the apoptosis induced by a withdrawal of  
RT NGF.";  
RL Biochem. Biophys. Res. Commun. 231:770-774(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/An;  
RX MEDLINE=97190206; PubMed=9038361;  
RA van de Craen M., Vandenabeele P., Declercq W., van den Brande I.,  
RA van Loo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,  
RA Fiers W.;  
RT "Characterization of seven murine caspase family members.";  
RL FEBS Lett. 403:61-69(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;  
RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATOR  
CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-  
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).  
CC CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE  
CC CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.  
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,  
CC KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND  
CC TESTIS.  
CC -1- PIM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE  
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND  
CC VICE VERSA (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
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CC EMBL; U54803; AAC52768.1; -  
 CC EMBL; U54802; AAC52768.1; JOINED.  
 CC EMBL; U49929; AAC52764.1; -  
 CC EMBL; D86352; BAA21727.1; -  
 CC EMBL; Y13086; CAA73528.1; -  
 CC EMBL; U19522; AAC5196.1; -  
 CC HSSP; P42574; 1PAU.  
 CC MEROPS; C14.003; -  
 CC MGD; MGI:107739; Casp3.  
 CC InterPro: IPR002398; ICE.  
 CC InterPro: IPR002138; ICE\_p10.  
 CC InterPro: IPR001309; ICE\_p20.  
 CC Pfam; PF00655; ICE\_p10; 1.  
 CC Pfam; PF00656; ICE\_p20; 1.  
 CC PRINTS; PR00376; ILBENZYM.  
 CC SMART; SM00115; CASc; 1.  
 CC PROSITE; PS01122; CASPASE\_CYS; 1.  
 CC PROSITE; PS01121; CASPASE\_HIS; 1.  
 CC PROSITE; PS50207; CASPASE\_P10; 1.  
 CC PROSITE; PS50208; CASPASE\_P20; 1.  
 CC KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.  
 CC FT PROPEP 1 9  
 CC FT PROPEP 1 28  
 CC FT CHAIN 29 175  
 CC FT CHAIN 176 277  
 CC FT ACT SITE 121 121  
 CC FT ACT SITE 163 163  
 CC FT CONFLICT 17 17  
 CC FT CONFLICT 51 51  
 CC FT CONFLICT 84 84  
 CC FT CONFLICT 95 95  
 CC FT CONFLICT 97 97  
 CC FT CONFLICT 128 128  
 CC FT CONFLICT 135 135  
 CC SEQUENCE 277 AA; 31474 MW; CE9159877482605 CRC64;  
 CC Query Match 20.4%; Score 276; DB 1; Length 277;  
 CC Best local Similarity 33.3%; Pred. No. 5e-14;  
 CC Matches 79; Conservativity 39; Mismatches 81; Indels 38; Gaps 9;  
 CC QY 35 ARGGEVDMEALERMFRYLKFEETMKRDPPTAQQLLEELDEFOQTDNWEKPVSCAFV-VL 93  
 CC DB 63 SRSGTVDVANDLRETFMGLKYQVANKNDLTREDILELMD---SVSKEDHSKRSSFCVCI 118  
 CC QY 94 MANGEGLGLGDEDEKWRLLDPLFVLANNNKCKARKPKRYIIIOACGHRDPDEELRGN 153  
 CC DB 119 LSHGDEGVITGTNGP-VELKKLTSPFGDYCRSLTGKPKFIIOACGTGLDCIE---- 173  
 CC QY 154 EELGDEBELGDEVAVLKNNPQSIPTDTLHISTVEGYLSYRHDKSGSGFIOTLD-- 211  
 CC DB 174 TDGCTDEMA-----CQKIPEADFLYAVSTAPGYISWNSKDSGFISLOSLMSL 223  
 CC QY 212 -VPIHKKGSILELTEETRLMANTENQESK-----PRKNVPEVOSTLRKKLY 258  
 CC DB 224 KLYAHK---LEFWMILTRV--NRKVATEFSFSLDSTFAKKQIPCIIVSLTKELY 274  
 CC RESULT 6  
 CC ICE2 HUMAN STANDARD; PRT; 435 AA.  
 CC AC P42575; P42576;  
 CC DT 01-NOV-1995 (Rel. 32, Created)  
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).

GN CASP2 OR ICH1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SSOURCE FROM N.A.  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=94373811; PubMed=8087842;  
 RA Wang L., Miura M., Bergeron L., Zhu H., Yuan J.;  
 RT "Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative  
 RT regulators of programmed cell death.";  
 RL Cell 78:739-750(1994).  
 RN [2]  
 RP CLEAVAGE SITES.  
 RX MEDLINE=96206041; PubMed=8654923;  
 RA Xue D., Shaham S., Hotvitz H.R.;  
 RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine  
 RT protease with substrate specificities similar to those of the human  
 RT CPP32 protease.";  
 RL Genes Dev. 10:1073-1083(1996).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER  
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING  
 CC PROTEINS NECESSARY FOR CELL SURVIVAL.  
 CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY  
 CC SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS. 2 ISOFORMS, ICH-1L (SHOWN HERE) AND ICH-1S;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER IN THE N-AND C-  
 CC TERMINI. ICH-1L ACTS AS A POSITIVE REGULATOR OF APOPTOSIS.  
 CC ICH-1S FUNCTIONS AS A NEGATIVE REGULATOR OF APOPTOSIS.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LARGER AMOUNTS IN THE EMBRYONIC  
 CC LUNG, LIVER AND KIDNEY THAN IN THE HEART AND BRAIN. IN THE ADULTS  
 CC HIGHER LEVEL EXPRESSION IS SEEN IN THE PLACENTA, LUNG, KIDNEY,  
 CC PANCREAS THAN IN THE HEART, BRAIN, LIVER AND SKELETAL MUSCLE.  
 CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT  
 CC THAT OF OTHER CASPASES.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
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CC EMBL; U13021; AAA58959.1; -  
 CC EMBL; U13022; AAA58960.1; -  
 CC HSSP; P29466; 1ICE.  
 CC MEROPS; C14.006; -  
 CC DB Genew; HGNC:1503; CASP2.  
 CC MIM; 60639; -  
 CC DR InterPro: IPR001315; CARD.  
 CC InterPro: IPR002398; ICE.  
 CC InterPro: IPR002138; ICE\_p10.  
 CC InterPro: IPR001309; ICE\_p20.  
 CC Pfam; PF00619; CARD; 1.  
 CC Pfam; PF00655; ICE\_p10; 1.  
 CC Pfam; PF00656; ICE\_p20; 1.  
 CC PRINTS; PR00376; ILBENZYM.  
 CC SMART; SM00114; CARD; 1.  
 CC SMART; SM00115; CASc; 1.  
 CC PROSITE; PS50209; CARD; 1.  
 CC PROSITE; PS01122; CASPASE\_CYS; 1.  
 CC PROSITE; PS01121; CASPASE\_HIS; 1.  
 CC PROSITE; PS50207; CASPASE\_P10; 1.  
 CC PROSITE; PS50208; CASPASE\_P20; 1.  
 CC KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.  
 CC FT PROPEP 1 152  
 CC FT CHAIN 153 308  
 CC FT PROPEP 309 316  
 CC CASPASE-2 SUBUNIT P18.

FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.  
 FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.  
 FT DOMAIN 15 103 CARD.  
 FT ACT SITE 260 260 BY SIMILARITY.  
 FT ACT SITE 303 303 BY SIMILARITY.  
 FT VARSPLIC 1 14 MISSING (IN ISOFORM ICH-1S).  
 FT VARSPLIC 306 435 DETDRGVDOODGKNHASPCEESDSDKEXLPKRLPTNSD  
 FT MLCVYKALLKGTAAAMRNKRGSGWYIEALQVSSRACDMHYA  
 FT PRCGRPT -> KGAIGSLGHLLEFTATASLAL (IN  
 FT ISOFORM ICH-1S).  
 FT MUTAGEN 303 303 C-2S: LOSS OF FUNCTION.  
 FT MUTAGEN 352 352 A-5T: LOSS OF FUNCTION.  
 SQ SEQUENCE 435 AA; 48855 MM; 1652EC73F6286FB7 CRC64;  
 Query Match 20.3%; Score 274.5; DB 1; Length 435;  
 Best Local Similarity 29.7%; Pred. No. 1,1e-13;  
 Matches 68; Conservative 51; Mismatches 103; Indels 7; Gaps 4;  
 QY 36 RESEVMEALERMPRYLKFEESTMKRDPDPAQOFLLEDEFOOTIDNWEPEVSCAFVILMA 95  
 DB 202 RSGGDVDSHTLVTLFKLGYDVHVLCDQTAQMOEKLQNFQO-LPAHRYVDSCLVALLS 259  
 QY 96 HGEGLTLKGEDEKRWLEDFEVLLNNKCKALRGKPKYV11QACGEHRDPGEELRGNEE 155  
 DB 260 HGVEGATVGVGKLLQLOEVFQLPNNANCPSLQNKPKKFFIQACGSDGTDRGVDOODGKN 319  
 QY 156 LGGBELAGDEVAIVAKNNPQSTPTTDLHLYSTVEGLSTRHDKSGGFLOTLDVPIH 215  
 DB 320 HAGSPGCEESDAGKEKLPKRLPTNSDMIQGYACLKGAAMNTRGSGWYIEALQVSE 379  
 QY 216 KKGS--ILELTEITRLMANTENVMOEGKP--RKVNPEVOSTLRKLYL 259  
 DB 380 RACDMHADVMLVKVALLKDRBGVAPGTBFHRCCKMSYECSTLCNHYL 428  
 RESULT 7  
 ICE3 RAT STANDARD: PRT: 277 AA.  
 AC P55213; P70543; Q62993; P97699;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama  
 protein) (CPP-32) (Caspase-3) (CASP-3) (SRBP cleavage activity 1)  
 DE (SCA-1) (LICE) (IRP).  
 GN CASP3 OR CPP32.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN NCBI  
 RN (1)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=96358624; PubMed=8761296;  
 RA Juan T.S.-C., McIniece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
 Fletcher F.A.;  
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding  
 a cysteine protease resembling Interleukin-1 beta converting enzyme  
 and CED-3.";  
 RT Oncogene 13:749-755 (1996).  
 RL (2)  
 RP SEQUENCE OF 30-241 FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=96042508; PubMed=7588240;  
 RA Flaws J.A., Kung K., Tirovich A.M., Desanti A., Tilly K.I.,  
 Hirschfeld A.N., Tilly J.L.;  
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and  
 mammalian cell death: dissociation of IRP-induced oligonucleosomal  
 endonuclease activity from morphological apoptosis in granulosa cells  
 of the ovarian follicle.";  
 RL Endocrinology 136:5042-5053 (1995).  
 RP (3)  
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain;  
 RX MEDLINE=97184204; PubMed=9030616;  
 RA M.B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,  
 RA Rosteck P. Jr., Politer G.G., Paul S.M.;  
 RT "Cloning and expression of a rat brain interleukin-1beta-converting  
 RT enzyme (ICE)-related protease (IRP) and its possible role in  
 RT apoptosis of cultured cerebellar granule neurons.";  
 RL J. Neurosci. 17:1561-1569 (1997).  
 RN (4)  
 RN SEQUENCE OF 1-264 FROM N.A.  
 RA Yakovlev A.G.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
 CC 216-ASP--GLY-217 BOND. CLEAVES AND ACTIVATES STEROID REGULATORY  
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-  
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE  
 CC BUT NOT IN KIDNEY OR TESTIS.  
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS  
 CC OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE  
 CC ADULT BRAIN.  
 CC -1- PTM: CLEAVAGE BY GRANTYME B, CASPASE-6, -8 AND -10 GENERATES THE  
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
 CC PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-7 PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND  
 CC VICE VERSA (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
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 CC  
 CC EMBL; U49930; AAC52765.1; -  
 CC EMBL; U34685; AAC52261.1; -  
 CC EMBL; U84410; AAB41792.1; -  
 CC EMBL; U58656; AAB02722.1; -  
 CC HSSP; P42574; 1PAU.  
 CC MEROPS; C14.003; -  
 CC InterPro; IPR002398; ICE.  
 CC InterPro; IPR002138; ICE\_P10.  
 CC InterPro; IPR001309; ICE\_P20.  
 CC Pfam; PF00655; ICE\_P10; 1.  
 CC Pfam; PF00656; ICE\_P20; 1.  
 CC PRINTS; PR00376; ILBENZYMIE.  
 CC SMART; SM00115; CASC; 1.  
 CC PROSITE; PS01122; CASPASE\_CYS; 1.  
 CC PROSITE; PS01121; CASPASE\_HIS; 1.  
 CC PROSITE; PS50207; CASPASE\_P10; 1.  
 CC PROSITE; PS50208; CASPASE\_P20; 1.  
 CC HydroLase; Thiol protease; Zymogen; Apoptosis.  
 KW PROPEP 1  
 FT PROPEP 10  
 FT CHAIN 29  
 FT CHAIN 176  
 FT ACT SITE 121  
 FT ACT SITE 121  
 FT ACT SITE 163  
 FT ACT SITE 25  
 FT CONFLICT 170  
 FT CONFLICT 178  
 FT CONFLICT 182  
 FT CONFLICT 187  
 FT CONFLICT 187  
 FT CONFLICT 190  
 FT CONFLICT 190  
 E -> G (IN REF. 3).

FT CONFLICT 199 199 T -> S (IN REF. 2).  
 FT CONFLICT 211 211 D -> G (IN REF. 2).  
 FT CONFLICT 236 236 L -> I (IN REF. 4).  
 FT CONFLICT 245 245 T -> M (IN REF. 3).  
 SO SEQUENCE 277 AA; 31491 MM; ADABF41BE2507402 CRC64;  
 Query Match 20.3%; Score 274; DB 1; Length 277;  
 Best Local Similarity 30.5%; Pred. No. 7e-14;  
 Matches 81; Conservative 44; Mismatches 93; Indels 48; Gaps 10;  
 QY 16 EERDMGARGALALVCTV-----KAREGSEVDMEALERFRVYLFESTMKRDPDTA 65  
 DB 34 DSSYKMYVPEGLCIIINNKNFKHSSTGSAANGDVDAANIRETFMALKYEVRRKNKDLTR 93  
 QY 66 QQFEELEDEFOOTIDNMEPEVSCAFV-VLMAGEEGELKGEDEKVRLEDFEVLNNNGC 124  
 DB 94 EIMELMD---SVSKEDSKRSSFCVYLISHGDEGVFTGNGP-VDLKULTSPFRGDCYC 148  
 QY 125 KALRGKPRVYIIQACRGEHRDPGEELRGNEELGDEELGDEGVAVLKNPNPSIPTTDTL 184  
 DB 149 RSLGKPRFLFIIOACRGTLEDCGIE---TDSGTDDMA-----CQKIPVADFL 194  
 QY 185 HIVEVGEVGLSYRDEKSGFGIQT---TDVFIKKSGILETEITRLMANTVMQSGK 241  
 DB 195 YAVSTAPGYSWRSRDSWFIQSICAMLKLYAHK---LEFMILITRV--NRKATEFE 248  
 QY 242 -----PRKNPEVOSTRKRLY 258  
 DB 249 SFSLDATPHAKQIPICTVSMITKELY 274  
 RESULT 8  
 ICE3 HUMAN STANDARD; PRT: 277 AA.  
 ID ICE3 HUMAN  
 AC P42574;  
 DT 01-NOV-1995 (Ref. 32, Created)  
 DT 01-NOV-1995 (Ref. 32, Last sequence update)  
 DT 15-JUN-2002 (Ref. 41, Last annotation update)  
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama  
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)  
 DE (SCA-1).  
 GN CASP3 OR CPP32.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).  
 RC TISSUE=T-cell;  
 RX MEDLINE=95074098; PubMed=7983002;  
 RA Fernandez-Alnemri T., Litwack G., Alnemri B.S.;  
 RT "CPP32, a novel human apoptotic protein with homology to  
 RT Interleukin-1 beta-converting enzyme."  
 RT J. Biol. Chem. 269:30761-30764(1994).  
 RL J. Biol. Chem. 269:30761-30764(1994).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95292347; PubMed=7774019;  
 RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,  
 RA Beldeir D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;  
 RA "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable  
 RT protease that cleaves the death substrate poly(ADP-ribose)  
 RT polymerase."  
 RT Cell 81:801-809(1995).  
 RL  
 RN  
 RP SEQUENCE OF 29-46 AND 175-193. AND FUNCTION.  
 RX MEDLINE=95319529; PubMed=7596430;  
 RA Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,  
 RA Gallant N.A., Gareau Y., Griffen P.R., Labelle M., Lazebnik Y.A.,  
 RA Munday N.A., Raju S.M., Smolton M.E., Yamin T.-T., Li V.L.,  
 RA Miller D.K.;  
 RT "Identification and inhibition of the ICE/CED-3 protease necessary  
 RT for mammalian apoptosis.";

RL Nature 376:37-43(1995).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.  
 RX MEDLINE=96266352; PubMed=8673606;  
 RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,  
 RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,  
 RA Thornberry N.A., Becker J.W.;  
 RT "The three-dimensional structure of apoptain/CPP32, a key mediator of  
 RT apoptosis."  
 RT Nat. Struct. Biol. 3:619-625(1996).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.  
 RX MEDLINE=97197830; PubMed=9045680;  
 RA Mitci P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,  
 RA Priestle J.P., Tomaselli K.J., Grutter M.G.;  
 RT "Structure of recombinant human CPP32 in complex with the  
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone";  
 RT J. Biol. Chem. 272:6539-6547(1997).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=20283632; PubMed=10821855;  
 RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,  
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,  
 RA Levy M.A., Dewolf W.E., Jr., Keller P.M., Tomaszek T., Head M.S.,  
 RA Ryan M.D., Hattiwanger R.C., Liang P.-H., Jamson C.A., McDevitt P.J.,  
 RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,  
 RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;  
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7  
 RT inhibit apoptosis and maintain cell functionality."  
 RT J. Biol. Chem. 275:16007-16014(2000).  
 RN [7]  
 RP PROCESSING.  
 RX MEDLINE=96353838; PubMed=8755496;  
 RA Fernandez-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,  
 RA Wang U., Bullrich F., Fritz U.C., Trapani J.A., Tomaselli K.J.,  
 RA Litwack G., Alnemri E.S.;  
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human  
 RT apoptotic cysteine protease containing two FADD-like domains";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).  
 RN [8]  
 RP CLEAVAGE OF HUNTINGTIN.  
 RX MEDLINE=96331285; PubMed=8696339;  
 RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,  
 RA Graham R.K., Brom M., Kazemi-Esfarjani P., Thornberry N.A.,  
 RA Vaillancourt J.P., Hayden M.R.;  
 RT "Cleavage of huntingtin by apoptain, a proapoptotic cysteine protease,  
 RT is modulated by the polyglutamine tract."  
 RT Nat. Genet. 13:442-449(1996).  
 RL  
 RN  
 RP FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
 CC PROTOCOLOGICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
 CC 216-ASP-|GLY-217 BOND. CLEAVES AND ACTIVATES SREBP. REGULATORY  
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-  
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE  
 CC CLEAVAGE OF HUNTINGTIN.  
 CC  
 CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.  
 CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (p17) AND A 12 kDa (p12) SUBUNIT.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER  
 CC AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW  
 CC IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN  
 CC CELLS OF THE IMMUNE SYSTEM.  
 CC  
 CC -1- PTM: CLEAVAGE BY GRANZYME B, ARAF-1, CASPASE-6, -8 AND -10  
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE  
 CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE  
 CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT  
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR  
 CC AND VICE VERSA.  
 CC  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC  
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DR EMBL; U13737; AAB65015.1; -  
DR EMBL; U13738; AAB60355.1; -  
DR EMBL; U26943; AAA74929.1; -  
DR PDB; 1PAU; 07-JUL-97.  
DR PDB; 1CE3; 24-DEC-97.  
DR PDB; 1GFW; 23-JUN-00.  
DR MEROPS; C14.003; -  
DR Genew; HGNC:1504; CASP3.  
DR MIM; 600636; -  
DR InterPro; IPR002398; ICE\_P10.  
DR InterPro; IPR002138; ICE\_P10.  
DR InterPro; IPR001309; ICE\_P10.  
DR Pfam; PF00655; ICE\_P10; 1.  
DR Pfam; PF00656; ICE\_P20; 1.  
DR PRINTS; PR00376; IL1BCENZYM.  
DR SMART; SMO0115; CASc; 1.  
DR PROSITE; PS01122; CASPASE\_CYS; 1.  
DR PROSITE; PS01121; CASPASE\_HIS; 1.  
DR PROSITE; PS50207; CASPASE\_P10; 1.  
DR PROSITE; PS50208; CASPASE\_P20; 1.  
KM Hydrolyase; Thiol protease; Zymogen; Apoptosis; Polymorphism;  
KM 3d-structure. 1  
FT PROPEP 1 9  
FT CHAIN 10 28  
FT CHAIN 29 175  
FT ACT\_SITE 176 277  
FT ACT\_SITE 121 121  
FT ACT\_SITE 163 163  
FT VARIANT 190 190  
SQ SEQUENCE 277 AA; 31594 MW; 8E34DD2ACE6EF64B CRC64;

Query Match 20.2%; Score 273; DB 1; Length 277;  
Best Local Similarity 31.5%; Pred. No. 8,4e-14;  
Matches 86; Conservative 41; Mismatches 104; Indels 42; Gaps 10;

QY 6 SEMSDPOLQOEERYDMGARGALALTLCTV-----ARCGSEVDMALERMRYLKF 55  
DB 24 SSMSSGSLDMSYMDYPMGCLITNNKHNKSTGMSRGTVDANLNFRLNLY 83  
QY 56 ESTMKRDPAAQFLBELDFOOTIDNMEPVCAPV-VLMHGEGLKGEDEKVRLED 114  
DB 84 EVRNKNDLTR---BEIVELMRDVSKEHSSKRSFVCVLLSHGEEGIIPTNGP-VDLKK 138  
QY 115 LFEVLNNKCKALRGKPKYIIQACGHRDPEELRGNEELGGDELDGDEFAVLKNNP 174  
DB 139 IINFRGDRCKSLTGKPKLFTIQACRGTLDCGIE---TDSGVD---DDMACKH--- 186  
QY 175 OSIPTYDTLHYSTVEGYLSYRHDEKSGFTQLTLDVFIHKKSGILLETETRLMANT 234  
DB 167 --IPVDADLVYSTAPGYVSWRNSKDSWFTQSLC-AMLKQYADLTFMHILTRV--NR 241  
QY 235 EVMQEGK-----PRKVNPEVOSTLRKKLY 258  
DB 242 KVATEFESFSPDATFPAKKQIPCIIVSMLTKELY 274

RESULT 9  
ICE3\_CRIL0 STANDARD; PRT; 277 AA.  
ID ICE3\_CRIL0  
AC Q60431;  
DT 01-NOV-1997 (Rel. 35, Last Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CP32) (Yama  
DE protein) (CSP-32) (Caspase-3) (SREBP cleavage activity 1)  
DE (SCA-1).

GN CASP3 OR CP32.  
OS Cricetus longicaudatus (long-tailed hamster) (Chinese hamster).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetus.  
NCBI Taxid=10030;

RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=9618185; PubMed=8605870;  
RA Wang X., Zelefski N.G., Yang J., Sakai J., Brown M.S.,  
RA Goldstein J.L.;  
RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by  
RT CP32 during apoptosis.";  
RL EMO J. 15:1012-1020(1996).

CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
CC 216-ASP-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY  
CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-  
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE  
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
CC PROPEPTASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
CC CASPASE-7 PROPEPTASE AND THE LARGE SUBUNIT OF CP32 ALSO OCCUR AND  
CC VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
CC  
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DR EMBL; U27463; AAB01511.1; -  
DR HSSP; P42574; 1PAU.  
DR MEROPS; C14.003; -  
DR InterPro; IPR002398; ICE\_P10.  
DR InterPro; IPR001309; ICE\_P10.  
DR InterPro; IPR002138; ICE\_P10.  
DR Pfam; PF00655; ICE\_P10; 1.  
DR Pfam; PF00656; ICE\_P20; 1.  
DR PRINTS; PR00376; IL1BCENZYM.  
DR SMART; SMO0115; CASc; 1.  
DR PROSITE; PS01122; CASPASE\_CYS; 1.  
DR PROSITE; PS01121; CASPASE\_HIS; 1.  
DR PROSITE; PS50207; CASPASE\_P10; 1.  
DR PROSITE; PS50208; CASPASE\_P20; 1.  
KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.  
KM 3d-structure. 1  
FT PROPEP 1 9  
FT CHAIN 10 28  
FT CHAIN 29 175  
FT CHAIN 176 277  
FT ACT\_SITE 121 121  
FT ACT\_SITE 163 163  
SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 19.5%; Score 263; DB 1; Length 277;  
Best Local Similarity 33.1%; Pred. No. 4,8e-13;  
Matches 78; Conservative 35; Mismatches 85; Indels 38; Gaps 9;

QY 36 RRGSEVDMALERMRYLKFESTMKRDPAAQFLBELDFOOTIDNMEPVCAPV-VLM 94  
DB 64 RSGTIVDAKRLRETMAKYEVRNNDLTR---BEIVELNNKSKAKHSSKRSFVCVIL 119  
QY 95 AHGEGLLKGEDEKVRLEDLFEVLNNKCKALRGKPKYIIQACGRHRDPEELRGNE 154

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Db 120 SHGEGVYFCTDGP-IDLKLTYSFRGDYCRSLIGKPKLFTIQACRGTELDCCGIETDSGT 178
Qy 155 ELGDEELGDEGVAVLKNPQSIPTYTDLHIYSTVEGYSYRHDENSGSPFIOTLT--- 211
Db 179 E-----DDMTC-----OKTVEADFLYAVSTAPYSYWRNPCKGSGWITQSLCSMLK 224
Qy 212 VFIHKGSILELTELTEIRLMANTEVMOEGK-----PRKAVPEVOSTLRKLY 258
Db 225 LVAMK-----LEPMILTRV--NRKVATEPESFSLDSTFHAKQIPCIYVSMULTKELY 274

RESULT 10
CED3 CAEVU STANDARD; PRT; 496 AA.
ID CED3 CAEVU
AC P45436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3.
OS Caenorhabditis vulgaria.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=31233;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94061982; PubMed=8242740.
RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
RT "The C. elegans cell death gene ced-3 encodes a protein similar to
RT mammalian interleukin-1 beta-converting enzyme."
RL Cell 75:641-652(1993).
CC -1- FUNCTION: ACTS AS A CYSTEINE PROTEASE IN CONTROLLING PROGRAMMED
CC CELL DEATH BY PROAPOPTOTICALLY ACTIVATING OR INACTIVATING A
CC SUBSTRATE PROTEIN OR PROTEINS, A POTENTIAL SUBSTRATE MAY BE CED-4.
CC ALTERNATIVELY IT MIGHT DIRECTLY CAUSE CELL DEATH BY
CC PROAPOPTOTICALLY CLEAVING PROTEINS THAT ARE CRUCIAL FOR CELL
CC VIABILITY (BY SIMILARITY).
CC -1- SUBUNIT: COULD BE A HETERODIMER OF TWO SUBUNITS DERIVED FROM THE
CC PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM.
CC -1- PTM: MAY BE REGULATED BY PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
DR HSSP; P42574; ICP3.
DR MEROPS: C14.002; -.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS; PR00376; ILICENZYM.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; zymogen; Apoptosis; Phosphorylation.
FT CHAIN 1 364 CELL DEATH PROTEIN 3 SUBUNIT 1
FT CHAIN 1 364 (POTENTIAL)
FT CHAIN 365 496 CELL DEATH PROTEIN 3 SUBUNIT 2
FT CHAIN 365 496 (POTENTIAL).
FT DOMAIN 1 91 CARD.
FT ACT_SITE 308 351 BY SIMILARITY.
FT ACT_SITE 351 351 BY SIMILARITY.
SQ SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;

Query Match 19.2%; Score 259.5; DB 1; Length 496;
Best Local Similarity 29.5%; Pred. No. 1.8e-12;
Matches 70; Conservative 52; Mismatches 96; Indels 19; Gaps 8;

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Qy 36 REGSEVMEALERMFRYLKEFESTKRPDPTAQOFLSEELDEFQGTIDNNEEPVSCAFVIMA 95
Db 253 RNRGKADKXDLTNIFRCMGV-TYICKNISGRGMLTTRDAKN-----ETHGDSALIVILS 307
Qy 96 HGEELGLKGEDEKVRLEDLFEVIANNNKALNGKPKVYIIQACRGHRDPG---EELR 151
Db 308 HGEENVIVIGVDVSVNHEIYDILLNANAPRLANKPKYLVEVQACRGGERDNGFPVLDSDV 367
Qy 152 GNEEL---GGDEELGDEGVAVLKNPQSIPTYTDLHIYSTVEGYSYRHDENSGSPFIOTLT 258
Db 368 GVPSLIRRGWMDNRDGPVFLCVRPQAOVWRKKRPSQADILIRATTAQVYSWRNSAGSGW 427
Qy 205 FIOTLTDFV-IHKKG-SILELTELRLMA-NTVEVMOEGKPRKVNPEVOSTLRKLY 258
Db 428 FIOAVCEVFSTHAKDMVVELLTVNKKVACGFTSGANILKQMPMTSLRLKKPF 484

RESULT 11
ICE7 HUMAN STANDARD; PRT; 303 AA.
ID ICE7 HUMAN
AC P55210; O13364; Q96BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-1-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CWH-1).
GN CASP7 OR MCH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
RA Dixit V.M.;
RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
RT factor-induced apoptosis."
RL J. Biol. Chem. 271:1621-1625(1996).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RC TISSUE=Spleen;
RX MEDLINE=96147144; PubMed=8567622;
RA Lipke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
RT cysteine protease similar to CPP32."
RL J. Biol. Chem. 271:1825-1828(1996).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
RC TISSUE=T-cell;
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salveson G.,
RA Barnshaw W.C., Litwack G., Alnemri E.S.;
RT "Wch3, a novel human apoptotic cysteine protease highly related to
RT CPP32."
RL Cancer Res. 55:6045-6052(1995).
RN [4]
RP SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS).
RC TISSUE=Fetal lung, and fetal spleen;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genome 40:86-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

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RN [6]  
 RP MEDLINE=96353838; PubMed=8755496;  
 RX Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,  
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomasselli K.J.,  
 RA Litwack G., Alnemri E.S.;  
 RT "In vitro activation of CPP32 and Mch3 by Mch3, a novel human  
 RT apoptotic cysteine protease containing two FAD-like domains";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).  
 CC -FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL  
 CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY  
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217  
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.  
 CC -ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.  
 CC -SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.  
 CC -SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -ALTERNATIVE PRODUCTS: 3 ISOFORMS; ALPHA (SHOWN HERE), BETA AND  
 CC ALPHA'; ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM IS  
 CC NOT PROTEOLYTICALLY ACTIVE.  
 CC -TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,  
 CC LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO  
 CC EXPRESSION IN THE BRAIN.  
 CC -PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE  
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY  
 CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND  
 CC VICE VERSA.  
 CC -SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF. 4 AS BETA.  
 CC BUT AS BETA IS ALREADY DEFINED IN REF. 3 WE HAVE CALLED IT ALPHA'.  
 CC -----  
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 CC -----  
 CC EMBL; U39613; AAC50346.1; -;  
 DR EMBL; U40281; AAC50352.1; -;  
 DR EMBL; U37448; AAC50303.1; -;  
 DR EMBL; U37449; AAC50304.1; -;  
 DR EMBL; U67319; AAC51152.1; -;  
 DR EMBL; U67320; AAC51153.1; -;  
 DR EMBL; U67206; AAF21460.1; -;  
 DR EMBL; BC015799; AAH15799.1; -;  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.004; -;  
 DR Genew; HGNC:1508; CASP7.  
 DR MIM; 601761; -;  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; ILIBCENZYM.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS0207; CASPASE\_P10; 1.  
 DR PROSITE; PS0208; CASPASE\_P20; 1.  
 KM Hydroxylase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.  
 FT PROPEP 1 23  
 FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.  
 FT PROPEP 199 206  
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.  
 FT ACT\_SITE 144 144 BY SIMILARITY.  
 FT ACT\_SITE 186 186  
 FT VARSPLIC 1 1  
 FT VARSPLIC 149 303 M -> MDCVGPDPGRKMKLEKNTSCGGSSGICASYVTOM  
 (IN ISOFORM ALPHA').  
 VIYKDGVTPIKDLTAHFGRDCKTLLEKPKLFITQACRG

FT FT ELDGQADSGPIINDPANPKYIPVEADPLFASTVPGY  
 FT FT SWRSRGSMFVQALCSILIEHGKDLLEIQTITLVNDRAR  
 FT FT HFSQSDDPHFHEKKQIPCVSMULTKELFSQ -> MESCS  
 FT FT VTQAGVQRDLGRLQPPPLPPLAAGPSILMAASRTPRPSMTQ  
 FT FT MLIDRSQWKLTSSSPPIPFQAITRGAGOEAPGLCKPSA  
 FT FT PSWRSTKMTKSCRSSPG (IN ISOFORM BETA).  
 FT FT C->A: NO APOPTOTIC ACTIVITY.  
 FT FT D -> E (IN REF. 5).  
 FT FT G -> A (IN REF. 1).  
 SQ SEQUENCE 303 AA; 34276 MW; CD373EE54A232CA4 CRC64;  
 Query Match 18.9%; Score 255.5; DB 1; Length 303;  
 Best Local Similarity 30.5%; Pred. No. 2e-12;  
 Matches 80; Conservative 41; Mismatches 100; Indels 41; Gaps 10;  
 QY 18 RYDMSGARLALTLCTVKT-----ARQSEYDMALRMFRYLKFESTMKRPTA-- 65  
 DB 59 QYNNMFELKGCITINNKNPFKVTGMGRNTRDADALFRCFSSLSGFDVIVYNDSCAK 118  
 QY 66 -QQLLEELDEFQOTIDWEEBVSQAFVVLMAHGEGLKDEKXVLEDLFEVLNNKNC 124  
 DB 119 MDDLKKAASEEDHT-----NAACFACILSHGSENVYKGD-GVPIKDLTAHFGRDRC 171  
 QY 125 KALGKPKVYITIQCRGHRDPGEELAGNEELGDEGLGDEVAVLKNPQ-SIPTYDPT 183  
 DB 172 KTLLEKPKLFPFIQACRGTELDG-----IQADSGPIINDTD---NPKYKIPVADP 219  
 QY 184 LHIYSTVEGYLSYRHDEKSGFIQTLTDVFIHKKGSILLETETRL---MANTEWQEG 240  
 DB 220 LFAVSTPGYISWMSPRGSMFVQALCSI-LEHNGKOLEIQILTRVNDRAHFEQSQD 278  
 QY 241 KP-----RKVNEVOSTLRKLY 258  
 DB 279 DPHFEKKQIPCVSMULTKELY 300  
 RESULT 12  
 ID ICE7 MOUSE STANDARD; PRT; 303 AA.  
 AC P97864; 008669;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic  
 DE protease Mch-3).  
 GN CASP7 OR MCH3 OR LICE2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=97224489; PubMed=9070923;  
 RA Juan T.S.-C., McIntee I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., Fletcher F.A.;  
 RT "Identification and mapping of Casp7, a cysteine protease resembling  
 RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";  
 RL Genomics 40:86-93(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97190206; PubMed=9038361;  
 RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,  
 RA Momoi T.;  
 RT "Mortaminin enhances CPP32-like activity during neuronal  
 RT differentiation of P19 embryonal carcinoma cells induced by retinoic  
 RT acid.";  
 RL Biochem. Biophys. Res. Commun. 232:192-197(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/An;  
 RX MEDLINE=97190206; PubMed=9038361;  
 RA van de Crieen M., Vandenberghe P., Declercq W., van den Brande I.,





DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; ILIBENZYM.E.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASc; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.  
 FT CHAIN 1 371  
 FT CHAIN 372 503  
 FT DOMAIN 1 91  
 FT ACT\_SITE 107 205  
 FT ACT\_SITE 304 304  
 FT ACT\_SITE 358 358  
 FT MUTAGEN 27 27  
 FT MUTAGEN 65 65  
 FT MUTAGEN 360 360  
 FT MUTAGEN 449 449  
 FT MUTAGEN 466 466  
 FT MUTAGEN 483 483  
 FT MUTAGEN 486 486  
 SQ SEQUENCE 503 AA; 56616 MM; 722D5831E94DMA69 CRC64;

Query Match 18.7%; Score 253; DB 1; Length 503;  
 Best Local Similarity 28.9%; Pred. No. 5,8e-12;  
 Matches 69; Conservative 49; Mismatches 101; Indels 20; Gaps 7;

QY 36 REGSEVDEMEALERMFRYLKFESESTMKRDPTAOQFLBELDEFQOITINWEEPSCAEVILMA 95  
 DB 259 RNCGTADNDNLNLRFCMGVYICNDNLGRGMLTLIRPAK---HEHGSGALIVILS 314  
 QY 96 HGEELKGEDEKMYRLLEFVLNNKCKALKRKRYIIACGEGHRDPGEELRGNEE 155  
 DB 315 HGEENVIIIGVDIPISTHEIYDLNNAANAPRLANKKIVFVACGERDNGFPVLDSVD 374  
 QY 156 -----LGDDELGG--DEVAVLNKNPQSI-----PTYDTLHISTVSGYSYHDEMG 202  
 DB 375 GVPARLRGMWRDPRDPLFELGCVPRQVOQVWRKPSQADILIAVATTAQVYVSWRNSARG 434  
 QY 203 SGFIOTLTVDF-IHKKG-SILELTERITRLMA-NTEVMQEGKPRKVPVQSTLRKLY 258  
 DB 435 SWFIQAVCEVFSTHAKDMVVELLTVNKKVACGFGTSGSNILKQMPMTSLRLKKFY 493

## RESULT 14

ICE9\_HUMAN STANDARD; PRT: 416 AA.  
 AC P55211.Q82852; Q95348; Q9U108; Q9UE03;  
 DT 01-OCT-1996 (Rel. 34; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic  
 DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease  
 DE activating factor 3) (APAF-3).  
 GN CASP9 OR MCH6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Primates; Catarrhini; Homindae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96279246; PubMed=8663294;  
 RA Duan H., Orth K., Chinnaiyan A.M., Poltier G.G., Froelich C.J.,  
 RA He W.-W., Dixit V.M.;

RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated  
 RT by the cytotoxic T cell protease granzyme B.";  
 RT J. Biol. Chem. 271:16720-16724(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. AND PROCESSING.  
 RC TISSUE=T-cell;  
 RX MEDLINE=97059171; PubMed=8900201;  
 RA Srinivasula S.M., Fernandes-Alnemri T., Zangwill J., Robertson N.,  
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,  
 RA Alnemri E.S.;  
 RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and  
 RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic  
 RT mediator CPP32.";  
 RL J. Biol. Chem. 271:27099-27106(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99315341; PubMed=10384055;  
 RA Hadano S., Nasir U., Nichol K., Raepers D.M., Vailancourt J.P.,  
 RA Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;  
 RT "Genomic organization of the human caspase-9 gene on chromosome  
 RT 1p36.1-p36.3.";  
 RL Mamm. Genome 10:757-760(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=99168502; PubMed=10070954;  
 RA Srinivasula S.M., Ahmed M., Guo Y., Zhan Y., Lazebnik Y.,  
 RA Fernandes-Alnemri T., Alnemri E.S.;  
 RT "Identification of an endogenous dominant-negative short isoform of  
 RT caspase-9 that can regulate apoptosis.";  
 RL Cancer Res. 59:999-1002(1999).  
 RN [5]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RC TISSUE=Stomach cancer;  
 RA Izawa M., Mori T., Ito H., Saitenji T.;  
 RT "Molecular cloning and sequencing of a cDNA predicting an alternative  
 RT form of pro-caspase-9 from human gastric cancer cell lines.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RA Mino Y., Momoi T., Fujita E.;  
 RT "A novel splicing product of human caspase-9 lacking protease  
 RT activity.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=99107856; PubMed=9890966;  
 RA Seol D.W., Billiar T.R.;  
 RT "A caspase-9 variant missing the catalytic site is an endogenous  
 RT inhibitor of apoptosis.";  
 RL J. Biol. Chem. 274:2072-2076(1999).  
 CC -I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE-9 TO APAF-  
 CC 1 LEADS TO ACTIVATION OF THE PROTEIN WHICH THEN CLEAVES AND  
 CC ACTIVATES CASPASE-3. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE)  
 CC POLYMERASE (PARP).  
 CC -I- FUNCTION: THE SHORT ISOFORM LACKS ACTIVITY IS AN DOMINANT-NEGATIVE  
 CC INHIBITOR OF CASPASE-9.  
 CC -I- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.  
 CC Caspase-9 and APAF1 bind to each other via their respective NH2-  
 CC terminal CED-3 homologous domains in the presence of cytochrome C  
 CC and ATP. Interacts with BIRC7.  
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG/9L/ALPHA FORM (SHOWN  
 CC HERE) AND A SHORT/9S/BETA FORM; ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -I- TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHEST EXPRESSION IN THE  
 CC HEART, MODERATE EXPRESSION IN LIVER, SKELETAL MUSCLE, AND  
 CC PANCREAS. LOW LEVELS IN ALL OTHER TISSUES.  
 CC -I- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32  
 CC GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 AND -10 CAN ALSO BE  
 CC INVOLVED IN THESE PROCESSING EVENTS.  
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -I- SIMILARITY: CONTAINS 1 CARD DOMAIN.



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DR EMBL; U56390; AAC50640.1; -  
 DR EMBL; U60521; AAC50766.1; -  
 DR EMBL; AB019305; BAA82697.1; -  
 DR EMBL; AB019197; BAA82697.1; JOINED.  
 DR EMBL; AB019198; BAA82697.1; JOINED.  
 DR EMBL; AB019199; BAA82697.1; JOINED.  
 DR EMBL; AB019200; BAA82697.1; JOINED.  
 DR EMBL; AB019201; BAA82697.1; JOINED.  
 DR EMBL; AB019202; BAA82697.1; JOINED.  
 DR EMBL; AB019203; BAA82697.1; JOINED.  
 DR EMBL; AB019204; BAA82697.1; JOINED.  
 DR EMBL; AF093130; AAD12248.1; -  
 DR EMBL; AB015653; BAA78780.1; -  
 DR EMBL; AB020979; BAA87905.1; -  
 DR EMBL; AF110376; AAD13615.1; -  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.010; -  
 DR Genew; HGNC:1511; CASP9.  
 DR MIM; 602234; -  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; IILBENZYM.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PSS0209; CARD; 1.  
 DR PROSITE; PSS0122; CASPASE\_CYS; 1.  
 DR PROSITE; PSS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PSS0207; CASPASE\_P10; 1.  
 DR PROSITE; PSS0208; CASPASE\_P20; 1.  
 DR HydroLase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.  
 KW PROPEP 1 ? 315 CASPASE-9 SUBUNIT P35.  
 FT CHAIN ? 315  
 FT PROPEP 316 330  
 FT CHAIN 331 416 CASPASE-9 SUBUNIT P10.  
 FT DOMAIN 1 92  
 FT ACT\_SITE 237 237 CARD.  
 FT ACT\_SITE 287 287 BY SIMILARITY.  
 FT VARSPIC 140 289 MISSING (IN SHORT ISOFORM).  
 FT CONFLICT 28 28 A -> V (IN REF. 1 AND 7).  
 FT CONFLICT 32 32 S -> R (IN REF. 1, 4, 5 AND 7).  
 FT CONFLICT 96 96 A -> G (IN REF. 1).  
 FT CONFLICT 197 197 P -> L (IN REF. 1).  
 FT CONFLICT 221 221 Q -> R (IN REF. 1).  
 SQ SEQUENCE 416 AA; 46195 MM; 874830FL1F8DC4CD CRC64;

Query Match 18.5%; Score 250; DB 1; Length 416;  
 Best Local Similarity 29.1%; Pred. No. 7,7e-12;  
 Matches 74; Conservative 46; Mismatches 90; Indels 44; Gaps 8;

QY 34 KARGSEVDMALRMPFYLFKESTMKRDPPTAQQLELDLFOOTIDWMEBPVSCAPVYL 93  
 DB 178 RTTGSNIDCKLRRRSSPHFWKBDLTKKKVLLALELAODHG--ALDCVVVI 234  
 QY 94 MANGE-----GLKGEDEKVRLEDLFEVLNNKCKALRGKPKVYIIQACRGERHP 146  
 DB 235 LSHCQASHLQFPQAVYCTDGCPSVVEKIVNIPNTSGPSLGGKPKLFFIACGGEQKDH 294  
 QY 147 GEELRGNEELGDELDGDEVALKNPQ-----SIPTTDTLHI 186  
 DB 295 GFEVASTSP--EDESP-----SNRPDPATFOEGLRTFDOLAISLPTSDIFVS 344

QY 187 YSTVEGLSYRHDKSGFIOTLDFVHKKSILEETIRLMANTVEQCKPRKN 246  
 DB 345 YSTPGVSMWMDPSSGMYWETLDDIF--EQWASSEDQLSLLVANA-VSKGIYKQM- 400  
 QY 247 PEVOSTLRKKLYLQ 260  
 DB 401 PGCFNPLRKLFFK 414

RESULT 15  
 ID7\_MESAU STANDARD; PRT; 303 AA.  
 AC P55214;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-7 precursor (BC 3.4.22.-) (ICE-1-like apoptotic protease 3)  
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)  
 DE (SCA-2).  
 GN CASP7 OR MCH3.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 ON NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RC STRAIN=Syrian; TISSUE=Liver;  
 RX MEDLINE=96224303; PubMed=8643593;  
 RA Pai J.-T., Brown M.S., Goldstein J.L.;  
 RT "Purification and cDNA cloning of a second apoptosis-related cysteine  
 RT protease that cleaves and activates sterol regulatory element binding  
 RT proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL  
 CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY  
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-[GLY-217  
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE  
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY  
 CC CPB32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPB32 PROTEASE ALSO OCCUR AND  
 CC VICE VERSA (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
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DR EMBL; U47332; AAC52595.1; -  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.004; -  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PR00376; IILBENZYM.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PSS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PSS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PSS0207; CASPASE\_P10; 1.  
 DR PROSITE; PSS0208; CASPASE\_P20; 1.

KM Hydrolase; Thiol protease; Zymogen; Apoptosis.  
FT PROPEP 1 23  
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.  
FT PROPEP 199 206 BY SIMILARITY.  
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.  
FT ACT\_SITE 144 144 BY SIMILARITY.  
FT ACT\_SITE 186 186 BY SIMILARITY.  
SQ SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match 18.5%; Score 249.5; DB 1; Length 303;  
Best Local Similarity 32.2%; Pred. No. 5.7e-12;  
Matches 76; Conservative 36; Mismatches 89; Indels 35; Gaps 9;

QY 36 REGSEVDMLEALERMFRYLKFESTMKRDPPTA---QQFLBELDEFQQTIDNWEEPVSCAFV 92  
DB 87 RNGTHDKDAEALFKCFRSLGFDVVYVNDSCAMQDLRKASEDHNS-----ACFACV 140  
QY 93 LMAHGEGLLKGDEKMWRLBDLFEVLNNKNCALRGKPKVYIIQACRGHRDPGEELRG 152  
DB 141 LLSHGEENLIYKGD-GVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDGVQ--- 196  
QY 153 NEELGDEBELGDEVAVLKNNPQ-SIPTYDTLHIYSTYEGYLSYRHDEKSGFIQTLD 211  
DB 197 -ADSGPINETDA-----NPRYKIPVEADFLPAYSTVPGYYSWRNPKGSMFVALCS 247  
QY 212 VFHHKGSILETEITRLMANTEVMQEGK-----PRKVNPEVOSTLRKKLY 258  
DB 248 I-LDEHGKDLIMQILIRV--NDRVARHFESEQDDPCFNEKKQIPQWVSMLTKEYL 300

Search completed: February 26, 2003, 12:19:25  
Job time : 9.80478 secs